

125082

From: Hamud, Fozia
Sent: Tuesday, December 27, 2005 12:34 PM
To: STIC-Biotech/ChemLib
Subject: sequence search 10/691,923

Hello,
Kindly search SEQ ID NO:34 of 10/691,923 against commercial and interference data bases. Thank you.

FOZIA HAMUD
PATENT EXAMINER
ART UNIT 1647
ROOM:REM 4D64
MAIL BOX: REM 4C70

URFF

Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: _____
Date completed: _____
Searcher Prep Time: _____
Online Time: _____

Type of Search
NA# _____ AA#: _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other (Specify): _____

GenCore version 5.1.6	32	83.5	8.7	414	2	Q69tn3	oryza sativ
Copyright (c) 1993 - 2005 Compugen Ltd.	33	83.5	8.7	499	2	Q4fbh3	eschierichia
OM protein - protein search, using sw model	34	83.5	8.7	597	2	Q7ul29	rhodopirell
Run on: December 29, 2005, 13:46:42 ; Search time 227 Seconds (without alignments)	35	83.5	8.7	716	2	Q6C489	yarrowia li
Title: US-10-691-923-34	36	83.5	8.7	1470	2	Q8chd4	mus musculu
Perfect score: 955	37	83	8.7	567	1	PCTA	homo sapien
Sequence: 1 MGPPVPTSKPTTNGKCHIGR. LKTVADGNLSLRSTTHPEST 182	38	83	8.7	567	2	Q6fhf7	homo sapien
Scoring table: BLOSUM62	39	83	8.7	567	2	Q5nvk5	pongo pygma
Gapop 10.0 , Gapext 0.5	40	83	8.7	579	2	Q8B711	mus musculu
Searched: 2166443 seqs, 705528306 residues	41	83	8.7	889	2	Q8DLX6	synchococc
Total number of hits satisfying chosen parameters: 2166443	42	82.5	8.6	1443	2	Q4t8k2	terratodon n
Minimum DB seq length: 0	43	82.5	8.6	3317	2	Q9RAHZ2	9NOSO
Maximum DB seq length: 2000000000	44	82	8.6	315	1	SPY2	MOUSE
Post-processing: Minimum Match 100%	45	82	8.6	899	1	PRP6	_YEAST
Database : UniProt 05.80;*							
1: uniprot_sprot:*							
2: uniprot_trembl:*							
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.							
SUMMARIES							
Result No.	Score	Query Match	Length	DB ID	Description		
1	945	99.0	200	1 IL29_HUMAN	Q8iu54	homo sapien	
2	667	69.9	200	1 IL28B_HUMAN	Q8iz19	homo sapien	
3	653	68.4	200	1 IL28A_HUMAN	Q8iz20	homo sapien	
4	477	49.9	193	2 Q4VK74_MOUSE	Q4vk74	mus musculu	
5	463	48.5	193	2 Q4VKT3_MOUSE	Q4vk73	mus musculu	
6	458	48.0	193	1 IL28_MOUSE	Q8cgk6	mus musculu	
7	97.5	10.2	692	1 PPK_ACIBA	Q9x4m8	acinetobact	
8	89	9.4	914	2 Q4ZV84_PSEY	Q4zv84	pseudomonas	
9	89	9.3	296	2 Q8G5G0_BIFLO	Q8g5g0	bifidobacte	
10	89	9.3	458	2 Q8DJL0_SYNEL	Q8dj0	synchococc	
11	88	9.3	313	2 Q75BW8_ASHGO	Q75bw8	ashbya goss	
12	87.5	9.2	953	2 Q6FCX8_ACIAD	Q6fcx8	acinetobact	
13	87	9.1	479	2 Q7OZJB_GITALA	Q7qzj8	giardia lam	
14	86	9.1	967	2 Q5B9M4_EMENI	Q5B9m4	aspergillus	
15	86	9.0	333	2 Q5BD46_BOVIN	Q5bd46	bos taurus	
16	86	9.0	528	2 Q4KB02_PSEFS	Q4kb02	pseudomonas	
17	86	9.0	567	2 Q5BAB0_BOVIN	Q5bab0	bos taurus	
18	85.5	9.0	574	2 Q52GV5_MAGGR	Q52gv5	magnaporthe	
19	85.5	9.0	2173	2 Q4Q895_LEIMA	Q4q895	leishmania	
20	85	8.9	673	2 Q57PJ5_SALCH	Q57pj5	salmonella	
21	85	8.9	975	2 Q4O6E0_LEIMA	Q4q6e0	leishmania	
				2 Q58P70_9RETR	Q58p70	small rumin	
				2 Q9SG79_ARABIDOPSIS	Q9sg79	arabidopsis	
				2 Q60AC8_METCA	Q60ac8	methylococc	
				2 Q884J3_PSEPM	Q884j3	pseudomonas	
				2 Q8J4V1_9RETR	Q8j4v1	viana/naedi	
				2 QDCK8_HUMAN	Q8nc50	homo sapien	
				2 Q5JPJ1_HUMAN	Q5jpj1	homo sapien	
				2 Q88N24_PSEPM	Q88n24	pseudomonas	
				2 Q9NV65_HUMAN	Q9nv65	homo sapien	
				2 Q7QEKS_ANOGA	Q7qek5	anopheles g	

PAHEY J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallius D.E., Schnierch A., Schein J.E., Jones S.J.M., Marrs M.A., "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences," Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

-!- FUNCTION: Cytokine with immunomodulatory activity. May play a role in antiviral immunity. Up-regulates MHC class I antigen expression. Ligand for the heterodimeric class II cytokine receptor composed of IL10RB and IL28RA. The ligand/receptor complex seems to signal through the Jak-STAT pathway.

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- INDUCTION: By viral infections or double stranded RNA.

CC -!- SIMILARITY: Belongs to the IL-28/IL-29 family.

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CC EMBL; AY129150; AAN28265.1; -; mRNA.

CC EMBL; AY184125.1; -; mRNA.

CC EMBL; AY1336716; AAR24511.1; -; mRNA.

CC EMBL; BC074985; AAT74985.1; -; mRNA.

CC Ensembl; ENSG00000182393; Homo sapiens.

CC HGNC; HNC018363; IL29.

CC MIM; 607403; .

CC KW Antiviral defense; Cytokine; Glycoprotein; Signal.

FT SIGNAL 1 19 Potential.

FT CHAIN 20 200 Interleukin 29.

FT CARBOHYD 65 65 N-linked (GlcNAc. . .) (Potential).

SQ SEQUENCE 200 AA; 21898 MW; D4333B9462DCB4A1 CRC64;

Query Match 2 GPVPTSKPRTGKGCHIGRKSLSPQELASFKKARDALLESLKLKNWCSSPVFPGNMDL 61

Best Local Similarity 99.4%; Score 94.0%; DB 1; Length 200; Matches 180; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 20 GPVPTSKPRTGKGCHIGRKSLSPQELASFKKARDALLESLKLKNWCSSPVFPGNMDL 79

Query Match 62 RLLQYRERPVALEELALTLKYLEAAAGPALEVDQDQPHTLHILSQLOQACIQOPTG 121

Best Local Similarity 99.4%; Score 94.0%; DB 1; Length 200; Matches 180; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 80 RLLQYRERPVALEELALTLKYLEAAAGPALEVDQDQPHTLHILSQLOQACIQOPTG 139

Query Match 122 PPRPGRPLHILRQDAPKESAGGLEASSTFNPLRLRDLKTVADGNLSLRSTHPPS 181

Best Local Similarity 99.4%; Score 94.0%; DB 1; Length 200; Matches 180; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 140 PPRPGRPLHILRQDAPKESAGGLEASSTFNPLRLRDLKTVADGNLSLRSTHPPS 199

Query Match 182 T 182

Db 200 T 200

RESULT 2

IL28B HUMAN

ID TI28B_HUMAN STANDARD PRT; 200 AA.

AC Q8I2I9; Q6VN56; Q724J3; Q8IWL6;

DT 01-FEB-2005 (Rel. 46, Created)

DT 01-FEB-2005 (Rel. 46, Last sequence update)

DT 13-SEP-2005 (Rel. 48, Last annotation update)

DE Interleukin 28B Precursor (IL-28B) (IL-28C) (Interferon lambda-3)

DE (IFN-lambda-3) (Interferon lambda-4) (IFN-lambda-4) (Cytokine ZC1022).

GN Name:IL28B; Synonym:IFNL3, IFNL4, IL28B, CYTO22;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Primates; Catarrhini; Hominidae;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini.

OC Homo.

NCBI_TaxID=9606;

OX RN [1] NUCLEOTIDE SEQUENCE, FUNCTION, AND INDUCTION.

RN RP PubMed=12469119; DOI=10.1038/n1873; RX

RN P. Kindtvoegel W., Xu W., Henderson K., Schlutzmeyer S., Shepard P., Kuestner R., Birks C., Roraback J., Whitmore T.E., Kuestner C., Dong D., Shin J., Presnall S., Fox B., Haledman B., Oberander C., Tackett M., Krivan W., Oberander C., Dong D., Gillett T., Grant F.J., Tackett M., McKnight G., Olegg C., Foster D., Klucher K.M.; RT "IL-28, IL-29 and their class II cytokine receptor IL-28R.";

RN [2] Nat. Immunol. 4:63-68 (2003).

RN NUCLEOTIDE SEQUENCE OF 5'-200, FUNCTION, SUBCELLULAR LOCATION, AND INDUCTION.

RN RP PubMed=12483210; DOI=10.1038/n1875; RX

RN Kortenko S.V., Gallagher G., Baurin V.V., Lewis-Antes A., Shen M., RA RA N.K., Langer J.A., Sheikh F., Donnelly R.P.; RT "IFN-lambdas mediate antiviral protection through a distinct class II cytokine receptor complex."

RN [3] Nat. Immunol. 4:69-77 (2003).

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RN P. Kindtvoegel W., Xu W., Henderson K., Schlutzmeyer S., Shepard P., Kuestner R., Birks C., Roraback J., Whitmore T.E., Kuestner C., Dong D., Shin J., Presnall S., Fox B., Haledman B., Oberander C., Tackett M., Krivan W., Oberander C., Dong D., Gillett T., Grant F.J., Tackett M., McKnight G., Olegg C., Foster D., Klucher K.M.; RT "IL-28, IL-29 and their class II cytokine receptor IL-28R.";

RN [2] Nat. Immunol. 4:63-68 (2003).

RN NUCLEOTIDE SEQUENCE OF 5'-200.

RN RP Li M., He S.; "Construction of mammalian cell expression vector of human interleukin IL-29, IL-28B and IL-28C gene from activated peripheral blood mononuclear cell and analysis of its sequence," Submitted (JUL-2003) to the EMBL/Genbank/DBJ databases.

RN P. Kindtvoegel W., Xu W., Henderson K., Schlutzmeyer S., Shepard P., Kuestner R., Birks C., Roraback J., Whitmore T.E., Kuestner C., Dong D., Shin J., Presnall S., Fox B., Haledman B., Oberander C., Tackett M., Krivan W., Oberander C., Dong D., Gillett T., Grant F.J., Tackett M., McKnight G., Olegg C., Foster D., Klucher K.M.; RT "IL-28, IL-29 and their class II cytokine receptor IL-28R.";

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RN [2] Nat. Immunol. 4:63-68 (2003).

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RN RP Li M., He S.; "Construction of mammalian cell expression vector of human interleukin IL-29, IL-28B and IL-28C gene from activated peripheral blood mononuclear cell and analysis of its sequence," Submitted (JUL-2003) to the EMBL/Genbank/DBJ databases.

RN P. Kindtvoegel W., Xu W., Henderson K., Schlutzmeyer S., Shepard P., Kuestner R., Birks C., Roraback J., Whitmore T.E., Kuestner C., Dong D., Shin J., Presnall S., Fox B., Haledman B., Oberander C., Tackett M., Krivan W., Oberander C., Dong D., Gillett T., Grant F.J., Tackett M., McKnight G., Olegg C., Foster D., Klucher K.M.; RT "IL-28, IL-29 and their class II cytokine receptor IL-28R.";

RN [2] Nat. Immunol. 4:63-68 (2003).

RN NUCLEOTIDE SEQUENCE OF 5'-200.

RN RP Li M., He S.; "Construction of mammalian cell expression vector of human interleukin IL-29, IL-28B and IL-28C gene from activated peripheral blood mononuclear cell and analysis of its sequence," Submitted (JUL-2003) to the EMBL/Genbank/DBJ databases.

RN P. Kindtvoegel W., Xu W., Henderson K., Schlutzmeyer S., Shepard P., Kuestner R., Birks C., Roraback J., Whitmore T.E., Kuestner C., Dong D., Shin J., Presnall S., Fox B., Haledman B., Oberander C., Tackett M., Krivan W., Oberander C., Dong D., Gillett T., Grant F.J., Tackett M., McKnight G., Olegg C., Foster D., Klucher K.M.; RT "IL-28, IL-29 and their class II cytokine receptor IL-28R.";

RN [2] Nat. Immunol. 4:63-68 (2003).

RN NUCLEOTIDE SEQUENCE OF 5'-200.

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RN P. Kindtvoegel W., Xu W., Henderson K., Schlutzmeyer S., Shepard P., Kuestner R., Birks C., Roraback J., Whitmore T.E., Kuestner C., Dong D., Shin J., Presnall S., Fox B., Haledman B., Oberander C., Tackett M., Krivan W., Oberander C., Dong D., Gillett T., Grant F.J., Tackett M., McKnight G., Olegg C., Foster D., Klucher K.M.; RT "IL-28, IL-29 and their class II cytokine receptor IL-28R.";

RN [2] Nat. Immunol. 4:63-68 (2003).

Db	144	QPTAGPRTRGRUHLHWLHQEAPKESSESGCLESVTNLFRLTRDNCVASSDL	198	Query Match 68.4%; Score 653.5%; DB 1; Length 200;
				Best Local Similarity 74.9%; Pred. No. 1.2e-51; Mismatches 131; Conservative 13; Gaps 2;
RESULT 3				
IL28A HUMAN	STANDARD;	PRT;	200 AA.	Qy 2 GPVPTSK---PTTGKCHIGKRFKLSPOELASFKKDALARESLKLKNWCSSESPVFGCN 58
ID Q8IZJ0	Q5VN55; Q8IWL7;			Db 24 GAVPVARIHLGALPDARGHIAQFKLSPOELAQFKDALARESLKLKNWCSSESPVFGCN 83
AC 08IZJ0				
DT 01-FEB-2005	(Rel. 46, Created)			
DT 01-FEB-2005	(Rel. 46, Last sequence update)			
DT 13-SEP-2005	(Rel. 48, Last annotation update)			
DB Interleukin 28A Precursor (IL-28A) (Interferon lambda-2) (IFN-lambda-2)				
DE (Cytokine 2CYT020)				
GN Name=IL28A; Synonyms=IFNL2, ZCYT020;				
OS Homo sapiens (Human).				
OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;				
OC Homo.				
OX NCBI_TaxID=9606;				
RN [1]				RESULT 4
RP NUCLEOTIDE SEQUENCE, FUNCTION, AND INDUCTION.				Q4VK74_MOUSE
RX PubMed=12469119; DOI=10.1038/ni873;				ID Q4VK74_MOUSE PRELIMINARY; PRT; 193 AA.
RA Sheppard P., Kindsvater W., Xu W., Henderson K., Schlutzmeyer S.,				AC Q4VK74;
RA Whitmore T.E., Kuestner R., Garrigues U., Biris C., Rorback J.,				DT 13-SEP-2005 (TREMBLrel. 31, Created)
RA Ostrander C., Dong D., Shin J., Presenell S., Fox B., Haldeman B.,				DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)
RA Cooper E., Taft D., Gilbert T., Grant F.J., Tackett M., Kriyan W.,				DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)
RA McKnight G., Clegg C., Poser D., Klucher K.M.; Nat.				DE Interferon-lambda2.
RA "IL-28, IL-29 and their class II cytokine receptor IL-28R.";				GN Name=ifnl2;
RL Nat. Immunol. 4:63-68(2003).				OS Mus musculus (Mouse).
RN [2]				OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
RP NUCLEOTIDE SEQUENCE OF 5'-200, FUNCTION, SUBCELLULAR LOCATION, AND				OC Mammalia; Eutheria; Euarchontoglires; Gires; Rodentia; Sciurognathi;
RX INDUCTION.				OC Muridae; Murine; Mus.
RX PubMed=12483210; DOI=10.1038/ni875;				OX NCBI_TaxID=10090;
RA Korenko S.V., Gallagher G., Baurin V.V., Lewis-Antes A., Shen M.,				RN [1]
RA Shah N.K., Langer J.A., Shaikh F., Dickensheets H., Donnelly R.P.,				RP NUCLEOTIDE SEQUENCE.
RT "IFN-lambdas mediate antiviral protection through a distinct class II				RC STRAIN=129/Sv;
CC cytokine receptor complex.";				RX PubMed=15948336; DOI=10.1099/vir.0.80904-0;
RL Nat. Immunol. 4:69-77(2003).				RA Bartlett N.W., Buttigieg K., Kotenko S.V., Smith G.L.;
RN [3]				RT "Murine interferon lambda (type III interferon) exhibit potent antiviral activity in vivo in a poxvirus infection model.";
RP NUCLEOTIDE SEQUENCE OF 4-200.				RL J. Gen. Virol. 86:1589-1596 (2005).
RA Li M., He S.;				DR AY86695; AAX5874-1; MW: 2538D2D710E9651F CRC64;
RT "Construction of mammalian cell expression vector of human interleukin (IL)-28A, IL-28B and IL-29 gene from activated peripheral blood mononuclear cell and analysis of its sequence.";				SQ SEQUENCE 193 AA; 21713 MW; Int. Immunopharmacol. 4:593-608 (2004).
RT Submitted (JUL-2003) to the EMBL/Genbank/DBJ databases.				RN [2]
CC -1- FUNCTION: Cytokine with immunomodulatory activity. May play a role in antiviral immunity. Up-regulates MHC class I antigen expression. Ligand for the heterodimeric class II cytokine receptor composed of IL10RB and IL28RA. The ligand/receptor complex seems to signal through the Jak-STAT pathway.				RP NUCLEOTIDE SEQUENCE.
CC -1- SUBCELLULAR LOCATION: Secreted.				RC STRAIN=129/Sv;
CC -1- INDUCTION: By viral infections or double stranded RNA.				RX PubMed=15948336; DOI=10.1099/vir.0.80904-0;
CC -1- SIMILARITY: Belongs to the IL-28/IL-29 family.				RA Bartlett N.W., Buttigieg K., Kotenko S.V., Smith G.L.;
CC -1- CAUTION: It is uncertain whether Met-1 or Met-5 is the initiator.				RT "Murine interferon lambda (type III interferon) exhibit potent antiviral activity in vivo in a poxvirus infection model.";
CC -1- This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.				RL J. Gen. Virol. 86:1589-1596 (2005).
CC -1- EMBL; AY129148; AN28263.1; -; mRNA.				DR AY86695; AAX5874-1; MW: 2538D2D710E9651F CRC64;
CC -1- EMBL; AY316715; AAR4510.1; ALT INIT; mRNA.				SQ SEQUENCE 193 AA; 21713 MW; Int. Immunopharmacol. 4:593-608 (2004).
DR Ensembl; ENSG0000183709; Homo sapiens.				RN [2]
DR HGNC; HGNC:18364; IL28A.				RP PRPRG-RHAMHLHRQEPKESAGCLEASATTFNLFRLTRDLYKAVADGN 170
DR MIM: 607401; -.				Db 141 PKPPSRLSRSLWHLHQEAQSKETPGCLEDSTVSNLFRLTRDLYKAVASGD 190
KW Antiviral defense; Cytokine; Signal.				
SIGNAL 1 25 Potential.				
FT CHAIN 26 200 Interleukin 28A.				
FT CONFLICT 151 151 T -> A (in Ref. 2).				
SQ SEQUENCE 200 AA; 22288 MW; DFC7B49P31BF488E CRC64;				
				RESULT 5
				Q4VK73_MOUSE
				ID Q4VK73_MOUSE PRELIMINARY; PRT; 193 AA.
				AC Q4VK73;
				DT 13-SEP-2005 (TREMBLrel. 31, Created)
				DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)
				DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)

DE Interferon-lambda3.
 GN Name=IL28; Synonyms=Ifnl3;
 OS Mus musculus (Mouse);
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Gires; Rodentia; Sciurognathi;
 OC Muridae; Murine; Mus.
 NCBI_TaxID=10500;
 [1]
 RN NUCLEOTIDE SEQUENCE.
 STRAIN=129/Sv;
 PubMed=15914836; DOI=10.1099/vir.0.80904-0;
 RA Bartlett N.W., Buttigieg K., Kotenko S.V., Smith G.L.;
 RT "Murine interferon lambda (type III interferon) exhibit potent
 antiviral activity in vivo in a Poxvirus infection model.";
 RL J. Gen. Virol. 96:1589-1596 (2005).
 MGI: MGI:2450574; AAX8715.1.; -; mRNA.
 DR EMBL: EMBL:AF116175; MGI:2450574;
 SQ SEQUENCE: 193 AA; 21690 MW; 9CBB2A3911F9B332 CRC64;
 LENGTH: 129; Score: 463; DB: 2; Length: 193;
 Best Local Similarity: 58.8%; Pred. No. 3.3e-24;
 Matches: 100; Conservative: 19; Mismatches: 49; Indels: 2; Gaps: 2;
 Qy 3 PVP-TSKPTTQGKCHIGRKFLSPLQELASPKKARDALESSILKLNWCSSPVFGNMDL 61
 Db 21 PVPTRPLPVAKDCIIAQFSLSPLQELQPKKADAEKRLLEDVRCSSHLISRMDL 80
 Qy 62 RLLQYERPVALEALATLKVLEBAAQPALEVDLQDPLTLHLHSQLOQCTQOPTAG 121
 Db 81 KQLOQERPVKAQAVLTKWENINDSALTTILQQLTLHSQLOQCTQOPTAG 140
 Qy 122 PRPRG-RLLHWLHLRQEAQPKKESAGCLEASVTFNIFRLTDLKTVADGN 170
 Db 141 PRPPSRLSRMLHLRQEAQSKEIPGCLEDSVTSNLFQLLRLKCVASGD 190

RESULT 6
 IL28 MOUSE STANDARD; PRT; 193 AA.
 ID IL28 MOUSE STANDARD; PRT; 193 AA.
 AC Q8CGK6;
 DT 01-FEB-2005 (Rel. 46, Created)
 DT 01-FEB-2005 (Rel. 46, Last sequence update)
 DT 13-SEP-2005 (Rel. 46, Last annotation update)
 DE Interleukin 28 precursor (Interferon lambda) (IFN-lambda).
 GN Name=IL28;
 OS Mus musculus (Mouse);
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Gires; Rodentia; Sciurognathi;
 OC Muridae; Murine; Mus.
 NCBI_TaxID=10500;
 RN NUCLEOTIDE SEQUENCE.
 STRAIN=IC57BL/6;
 PubMed=12483210; DOI=10.1038/ni875;
 RA Kotenko S.V., Gallagher G., Baurin V.V., Lewis-Antes A., Shen M.,
 RA Shah N.K., Langer J.A., Sheikh F., Dickensheets H., Donnelly R.P.,
 RT "IFN-lambda mediate antiviral protection through a distinct class II
 cytokine receptor complex.";
 RL Immunol. 4:69-77 (2003).
 CC -!- FUNCTION: Cytokine with immunomodulatory activity. May play a role
 CC in antiviral immunity. Up-regulates MHC class I antigen
 CC expression. Ligand for the heterodimeric class II cytokine
 CC receptor composed of IL10RB and IL22RA. The ligand/receptor
 CC complex seems to signal through the Jak-STAT pathway (By
 CC similarity).
 CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).

CC -!- SIMILARITY: Belongs to the IL-28/IL-29 family.
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC EMBL; AY184375; AAN86128.1.; -; mRNA.
 DR Ensembl; ENSMUSG00000066747; Mus musculus.
 DR MGI; MGI:2450574; I128.
 KW Antiviral defense; Cytokine; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 193 AA; 21664 MW; 357A000AACABC61 CRC64;
 SQ SEQUENCE 193 AA;
 DR Query Match 48.0%; Score: 458; DB: 1; Length: 193;
 DR Best Local Similarity 58.2%; Pred. No. 9.4e-34;
 DR Matches 99; Conservative 19; Mismatches 50; Indels 2; Gaps 2;
 DR SIGNAL 1 19
 DR 3 PVP-TSKPTTQGKCHIGRKFLSPLQELASPKKARDALESSILKLNWCSSPVFGNMDL 61
 DR 21 PVPTRPLPVAKDCIIAQFSLSPLQELQPKKADAEKRLLEDVRCSSHLISRMDL 80
 DR 62 RLLQYERPVALEALATLKVLEBAAQPALEVDLQDPLTLHLHSQLOQCTQOPTAG 121
 DR 81 KQLOQERPVKAQAVLTKWENINDSALTTILQQLTLHSQLOQCTQOPTAG 140
 DR 122 PRPRG-RLLHWLHLRQEAQPKKESAGCLEASVTFNIFRLTDLKTVADGN 170
 DR 141 PRPPSRLSRMLHLRQEAQSKEIPGCLEDSVTSNLFQLLRLKCVASGD 190
 RESULT 7
 PPK ACIBA STANDARD; PRT; 692 AA.
 ID PPK ACIBA STANDARD; PRT; 692 AA.
 AC Q9XKMB;
 AC DT 16-OCT-2001 (Rel. 40, Created)
 AC DT 16-OCT-2001 (Rel. 40, Last sequence update)
 AC DT 13-OCT-2005 (Rel. 48, Last annotation update)
 AC DT 13-SEP-2005 (Rel. 48, Last sequence update)
 AC DE Polyphosphate kinase (EC 2.7.4.1). (Polyphosphoric acid kinase) (ATP-
 DE polyphosphate phosphotransferase).
 GN Name=ppk;
 AC Acinetobacter baumannii;
 AC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 AC Moraxellaceae; Acinetobacter.
 OC NCBI_TaxID=470;
 RN [1]_TaxID=470;
 RN NUCLEOTIDE SEQUENCE [GENOMIC DNA].
 RC STRAIN=232;
 RC MEDLINE=20005507; PubMed=10527215;
 RX Gavigan J.A., Marshall L.M., Dobson A.D.W.;
 RA RT "Regulation of polyphosphate kinase gene expression in Acinetobacter
 RA baumannii 252.";
 RA Microbiology 145:2931-2937 (1999).
 RL RT -!- FUNCTION: Catalyzes the reversible transfer of the terminal
 CC phosphate of ATP to form a long-chain polyphosphate (polyP).
 CC -!- CATALYTIC ACTIVITY: ATP + (phosphate) (n) = ADP + (phosphate) (n+1).
 CC -!- CPTM: An intermediate of this reaction is the autophosphorylated
 CC ppk in which a phosphate is covalently linked to histidine
 CC -!- SIMILARITY: Belongs to the polyphosphate kinase family.
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC EMBL; AF116175; AAD28429.1.; -; Genomic_DNA.
 DR HAMAP; MF_00347.; 1.
 DR InterPro; IPR00341.; PP_kinase.
 DR Pfam; PF02503; PP_kinase; 1.
 DR

KW	Phosphorylation; Transferase.	
FT ACT_SITE	443	443 Phosphohistidine intermediate (By similarity).
FT ACT_SITE	462	462 Phosphohistidine intermediate (By similarity).
FT SEQUENCE	692 AA;	78980 MW; C7EB0011DF332920 CRC64;
Query Match	Score 10.2%; DB 1; Length 92;	
Best Local Similarity	22.6%; Pred. No. 4.5%;	
Matches	24 LSPQELAS--FKKARDALEESLKLKWNKSCSSPVFGNWLRLQVRERPVAL-----E 74	Qy 108 SLOQACIQQPTAGPRPRGLRHLHR-----LQEAKPKESAGCL-EASVTFN 154
Qy	85 LSPQEILHQSSETAHAALEHQYQILN---EQIPP-----QLRREGISFLRRGELTQ 132	Db 481 NEMQAGRLDRPALAVNFTSLIPNWLDSEHFTPDLKVLALYGANRHODGNLQDYLIL 540
Db	75 ASBLATLURKVLREAAAGPAEDVLDQPLH-----TLLHILS-----LQEACIQPO 117	Qy 155 LFRLLTDRDK 164
Qy	133 AQSNTWVKKYFQEQVAPALTPISLDPAHFPRLVNSKINFIVLEGDAFGQDILAVVA 192	Db 541 TYALPDRLE 550
Qy	118 PTAGPR-----PRGRLLHML-----HRLQEAKPKESAGCLESASVTFNLFRLTLD 162	RESULT 9
Db	193 PHSLPRVVRLPDLETEKHHVMLSS1IHTAVSDSPFGMTATGCVQFRVTNADLTLD 252	Q8G5G0_BIFIO
Qy	163 LKYVAD 168	ID Q8G5G0_BIFIO PRELIMINARY;
Db	253 VEDLAE 258	AC Q8G5G0;
Qy	42784 PSESY PRELIMINARY; PRT; 914 AA.	DT 01-MAR-2003 (TrEMBLrel. 23, Created)
Db	42784 PSESY PRELIMINARY; PRT; 914 AA.	DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
RESULT 8		DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Q42784	Q42784 PSESY PRELIMINARY; PRT; 914 AA.	DE Hypothetical protein.
AC	Q42784-2005 (TrEMBLrel. 31, Created)	GN OrderedLocusNames=BL1052;
DT	13-SEP-2005 (TrEMBLrel. 31, Last sequence update)	OS Bifidobacterium longum.
DT	13-SEP-2005 (TrEMBLrel. 31, Last annotation update)	OC Bacterium: Actinobacteriae; Actinobacteridae; Bifidobacteriales;
DE	SNP2-related:Helicase, C-terminal:SWIM Zn-finger.	OC Bifidobacteriaceae; Bifidobacterium.
GN	Names=syR_1894;	RN [1]
OS	Pseudomonas syringae pv. syringae B728a.	RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;	RC STRAIN=NCC 2705;
OC	Pseudomonadaceae; Pseudomonas.	RA MEDLINE=22294977; PubMed=12381787; DOI=10.1073/pnas.212527599;
OX		RA Schein M.A., Karmirantzou M., Snel B., Vilanova D., Berger B.,
[1]	NCBI_TAXID=205918;	RA Pessi G., Zwalien M.-C., Desiere F., Bork P., Delley M.,
RP	NUCLEOTIDE SEQUENCE.	RA "The genome sequence of Bifidobacterium longum reflects its adaptation to the human gastrointestinal tract";
RC	DOI Joint Genome Institute;	RL Proc. Natl. Acad. Sci. U.S.A. 99:14422-14427 (2002).
RA	Chain A., Larimer F., Bartolo G., Copeland A., Lykidis A., Trong S.,	DR EMBL: AE014295; AAC24858.1; -; Genomic DNA.
RA	Nolan M., Gotsman E., Thiel J., Malfatti S., Lapidot A., Detter J.C.,	KW Complete proteome; Hypothetical protein.
RA	Land M., Richardson P.M., Kyrpides N.C., Ivanova N.;	SQ SEQUENCE 296 AA; 33881 MW; 5429BC632765994E CRC64/
RT	Comparison of two complete genome sequences of <i>Pseudomonas syringae</i> pv. <i>syringae</i> B728a and pv. <i>tomato</i> DC3000.;"	Query Match 9.3%; Score 89; DB 2; Length 296;
RL	Proc. Natl. Acad. Sci. U.S.A. 0:0-(2005).	Best Local Similarity 28.9%; Pred. No. 9.8%;
RN	NUCLEOTIDE SEQUENCE.	Matches 39; Conservative 19; Missmatches 55; Indels 22; Gaps 8;
[2]	STRAIN=B728a;	Qy 46 KNW-SCSSPVPGNWDLRL-LQVRERPVALEELALTLYEAAG-----PALEVDVL 97
RC	DOI Joint Genome Institute;	Db 14 RTWRCRTPAEPDRDVKRLLAARAHKFRQVRDDVLTRHLELREGLETLICVDAID 73
RA	Chai A., Larimer F., Bartolo G., Copeland A., Lykidis A., Trong S.,	Qy 98 QPLTFLHILSOLQRCIOQPTAEPPR-GRLHFLHLRQEAKPKESAGCLEASVTFN 155
RA	Nolan M., Gotsman E., Thiel J., Malfatti S., Lapidot A., Detter J.C.,	Db 74 GPAQTRLRLKLPVGVTR-TGAFLPRTGACHRLHILRKG-----IEHPLFEEH 124
RA	Land M., Richardson P.M., Kyrpides N.C., Ivanova N.;	Qy 156 PRLLTDLKTVADGN 170
RT	Comparison of two complete genome sequences of <i>Pseudomonas syringae</i> pv. <i>syringae</i> B728a and pv. <i>tomato</i> DC3000.;"	Db 125 AR--NRD-ROVDDGD 136
RL	Proc. Natl. Acad. Sci. U.S.A. 0:0-(2005).	RESULT 10
RN	NUCLEOTIDE SEQUENCE.	Q8D0L0_SYNEL
RC	STRAIN=B728a;	ID Q8D0L0_SYNEL PRELIMINARY;
RA	Peil H., Peil W.S., Lindow S.E.;	AC Q8D0L0;
RA	Submitted (MAY-2005) to the EMBL/GenBank/NCBI databases.	DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DR	EMBL: CP000075; AAC36938.1; -; Genomic DNA.	DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DR	GO:GO:0004386; F:Helicase activity; IEA.	DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
RW	SEQUENCE 914 AA; 104114 MW; 3C9DD8894DFB4B5B CRC64;	DE Isochordismate synthase.
RN		GN OrderedLocusNames=BL11213;
[3]	NUCLEOTIDE SEQUENCE.	OS <i>Synechococcus elongatus</i> (Thermosynechococcus elongatus).
RP	STRAIN=B728a;	OC Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
RC	Submitted (MAY-2005) to the EMBL/GenBank/NCBI databases.	RN [1]
RN		RP STRAIN=BP-1;
RP	NUCLEOTIDE SEQUENCE.	RC MEDLINE=2222144; PubMed=12240834;
RC	STRAIN=B728a;	RA Watanabe A., Kaneko T., Sato S., Ikeuchi M., Katoh H., Sasamoto S.,
RA	Peil H., Peil W.S., Lindow S.E.;	RA Kishida Y., Kohara M., Matsunoto M., Nakazaki N.,
RA	Submitted (MAY-2005) to the EMBL/GenBank/NCBI databases.	Kiyokawa C., Kohara M., Matsunoto M., Nakazaki N.,
DR	EMBL: CP000075; AAC36938.1; -; Genomic DNA.	
DR	GO:GO:0004386; F:Helicase activity; IEA.	
RW	SEQUENCE 914 AA; 104114 MW; 3C9DD8894DFB4B5B CRC64;	
Qy	62 RLLQVRERPVALEELALTLY-----VLEAAAGPALED-----VLDQPLHILHHL 107	Query Match 9.4%; Score 89.5%; DB 2; Length 914;
Db	421 RLNIKDAVPSLPLDGLNATLPYQLEGISWMQSLRELEYGGVLADDMGIGKGTQTLAHL 480	Best Local Similarity 26.2%; Pred. No. 33; Missmatches 50; Indels 27; Gaps 4;

RA	Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.; "Complete genome structure of the thermophilic cyanobacterium RL Thermosynechococcus elongatus BP-1.";	Db	138	-----	-----	-----	-----	-----
RT	EMBL: BA000039; (2002).	RT	Q6FCX8_ACIAD	ACTAD PRELIMINARY;	PRT;	953 AA.		
DR	HSSP: P05041; 1KG	ID	Q6FCX8_ACIAD					
GO	GO:0008909; P: isochorismate synthase activity; IEA.	AC	Q6FCX8_ACIAD					
InterPro	IPR005801; Anth synth chor.	DT	06FCX8_ACIAD					
DR	IPR00581; Isochoror synth.	DT	05-JUL-2004	(TREMBLrel. 27, Created)				
Pfam	Pf0025; Chorismate bind; 1.	DT	05-JUL-2004	(TREMBLrel. 27, Last sequence update)				
PIRSF	PIRSF001502; Isochorismt synth; 1.	DB	RNA helicase.					
ProDom	PP0000729; Anth synth Chor; 1.	GN	Name-hepA; OrderedlocusNames=ACIAD1204;					
TIGRFAMs	TIGR00543; isochoror_synth; 1.	OS	Acinetobacter sp. (strain ADP1).					
KW	Complete proteome.	OC	Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Moraxellaceae; Acinetobacter.					
SEQUENCE	458 AA; 51214 MW; B289D125D60428E3 CRC64;	NCBI_TaxID=62977;	OX					
		[1]	RN					
			RP	NUCLEOTIDE SEQUENCE.				
			RC	STRAIN=ADP1;				
			RA	PubMed:15514110; DOI=10.1093/nar/gkh910;				
			RA	Barbe V., Valenet D., Fonckenhen N., Kreinmeyer A., Oztas S.,				
			RA	Labarre L., Crueviller S., Robert C., Duprat S., Wincher P.,				
			RA	Ornston L.N., Weissenbach J., Mariere P., Cohen G.N., Medigue C.;				
			RT	"Unique features revealed by the genome sequence of <i>Acinetobacter</i> sp. ADP1, a versatile and naturally transformation competent bacterium."				
			RL	Acids Res. 32:566-5779 (2004).				
			DR	EMBL: CR53861; CAG68081.1; -; Genomic DNA.				
			DR	GO:0054824; F:AMP binding; IEA.				
			DR	GO:003677; F:DNA binding; IEA.				
			DR	GO:004386; F:helicase activity; IEA.				
			DR	GO:0015668; F:type III site-specific deoxyribonuclease ac. . .; IEA.				
			DR	GO:0009307; P:DNA restriction; IEA.				
			DR	InterPro: IPR011545; DEAD/DEAH N.				
			DR	InterPro: IPR016150; Helicase_C.				
			DR	InterPro: IPR003330; SNF2_N.				
			DR	Pfam: PF00271; Helicase_C; 1.				
			DR	Pfam: PF00176; SNP2_N; 1.				
			DR	SMART: SM00487; DEAD_C; 1.				
			DR	SMART: SM00490; HELICC; 1.				
			KW	Complete proteome; Helicase.				
			DR	SEQUENCE 953 AA; 109300 MW; C7C160A9C8105721 CRC64;				
			DR	Best Local Similarity 9.2%; Score 87.5; DB 2; Length 953;				
			DR	Matches 40; Conservative 30; Mismatches 71; Indels 39; Gaps 7;				
			DR	InterPro: IPR0161545; DEAD/DEAH N.				
			DR	InterPro: IPR016150; Helicase_C.				
			DR	InterPro: IPR003330; SNF2_N.				
			DR	Pfam: PF00271; Helicase_C; 1.				
			DR	Pfam: PF00176; SNP2_N; 1.				
			DR	SMART: SM00487; DEAD_C; 1.				
			DR	SMART: SM00490; HELICC; 1.				
			KW	Complete proteome; Helicase.				
			DR	SEQUENCE 953 AA; 109300 MW; C7C160A9C8105721 CRC64;				
			DR	Best Local Similarity 9.2%; Score 87.5; DB 2; Length 953;				
			DR	Matches 40; Conservative 30; Mismatches 71; Indels 39; Gaps 7;				
			DR	InterPro: IPR0161545; DEAD/DEAH N.				
			DR	InterPro: IPR016150; Helicase_C.				
			DR	InterPro: IPR003330; SNF2_N.				
			DR	Pfam: PF00271; Helicase_C; 1.				
			DR	Pfam: PF00176; SNP2_N; 1.				
			DR	SMART: SM00487; DEAD_C; 1.				
			DR	SMART: SM00490; HELICC; 1.				
			KW	Complete proteome; Helicase.				
			DR	SEQUENCE 953 AA; 109300 MW; C7C160A9C8105721 CRC64;				
			DR	Best Local Similarity 9.2%; Score 87.5; DB 2; Length 953;				
			DR	Matches 40; Conservative 30; Mismatches 71; Indels 39; Gaps 7;				
			DR	InterPro: IPR0161545; DEAD/DEAH N.				
			DR	InterPro: IPR016150; Helicase_C.				
			DR	InterPro: IPR003330; SNF2_N.				
			DR	Pfam: PF00271; Helicase_C; 1.				
			DR	Pfam: PF00176; SNP2_N; 1.				
			DR	SMART: SM00487; DEAD_C; 1.				
			DR	SMART: SM00490; HELICC; 1.				
			KW	Complete proteome; Helicase.				
			DR	SEQUENCE 953 AA; 109300 MW; C7C160A9C8105721 CRC64;				
			DR	Best Local Similarity 9.2%; Score 87.5; DB 2; Length 953;				
			DR	Matches 40; Conservative 30; Mismatches 71; Indels 39; Gaps 7;				
			DR	InterPro: IPR0161545; DEAD/DEAH N.				
			DR	InterPro: IPR016150; Helicase_C.				
			DR	InterPro: IPR003330; SNF2_N.				
			DR	Pfam: PF00271; Helicase_C; 1.				
			DR	Pfam: PF00176; SNP2_N; 1.				
			DR	SMART: SM00487; DEAD_C; 1.				
			DR	SMART: SM00490; HELICC; 1.				
			KW	Complete proteome; Helicase.				
			DR	SEQUENCE 953 AA; 109300 MW; C7C160A9C8105721 CRC64;				
			DR	Best Local Similarity 9.2%; Score 87.5; DB 2; Length 953;				
			DR	Matches 40; Conservative 30; Mismatches 71; Indels 39; Gaps 7;				
			DR	InterPro: IPR0161545; DEAD/DEAH N.				
			DR	InterPro: IPR016150; Helicase_C.				
			DR	InterPro: IPR003330; SNF2_N.				
			DR	Pfam: PF00271; Helicase_C; 1.				
			DR	Pfam: PF00176; SNP2_N; 1.				
			DR	SMART: SM00487; DEAD_C; 1.				
			DR	SMART: SM00490; HELICC; 1.				
			KW	Complete proteome; Helicase.				
			DR	SEQUENCE 953 AA; 109300 MW; C7C160A9C8105721 CRC64;				
			DR	Best Local Similarity 9.2%; Score 87.5; DB 2; Length 953;				
			DR	Matches 40; Conservative 30; Mismatches 71; Indels 39; Gaps 7;				
			DR	InterPro: IPR0161545; DEAD/DEAH N.				
			DR	InterPro: IPR016150; Helicase_C.				
			DR	InterPro: IPR003330; SNF2_N.				
			DR	Pfam: PF00271; Helicase_C; 1.				
			DR	Pfam: PF00176; SNP2_N; 1.				
			DR	SMART: SM00487; DEAD_C; 1.				
			DR	SMART: SM00490; HELICC; 1.				
			KW	Complete proteome; Helicase.				
			DR	SEQUENCE 953 AA; 109300 MW; C7C160A9C8105721 CRC64;				
			DR	Best Local Similarity 9.2%; Score 87.5; DB 2; Length 953;				
			DR	Matches 40; Conservative 30; Mismatches 71; Indels 39; Gaps 7;				
			DR	InterPro: IPR0161545; DEAD/DEAH N.				
			DR	InterPro: IPR016150; Helicase_C.				
			DR	InterPro: IPR003330; SNF2_N.				
			DR	Pfam: PF00271; Helicase_C; 1.				
			DR	Pfam: PF00176; SNP2_N; 1.				
			DR	SMART: SM00487; DEAD_C; 1.				
			DR	SMART: SM00490; HELICC; 1.				
			KW	Complete proteome; Helicase.				
			DR	SEQUENCE 953 AA; 109300 MW; C7C160A9C8105721 CRC64;				
			DR	Best Local Similarity 9.2%; Score 87.5; DB 2; Length 953;				
			DR	Matches 40; Conservative 30; Mismatches 71; Indels 39; Gaps 7;				
			DR	InterPro: IPR0161545; DEAD/DEAH N.				
			DR	InterPro: IPR016150; Helicase_C.				
			DR	InterPro: IPR003330; SNF2_N.				
			DR	Pfam: PF00271; Helicase_C; 1.				
			DR	Pfam: PF00176; SNP2_N; 1.				
			DR	SMART: SM00487; DEAD_C; 1.				
			DR	SMART: SM00490; HELICC; 1.				
			KW	Complete proteome; Helicase.				
			DR	SEQUENCE 953 AA; 109300 MW; C7C160A9C8105721 CRC64;				
			DR	Best Local Similarity 9.2%; Score 87.5; DB 2; Length 953;				
			DR	Matches 40; Conservative 30; Mismatches 71; Indels 39; Gaps 7;				
			DR	InterPro: IPR0161545; DEAD/DEAH N.				
			DR	InterPro: IPR016150; Helicase_C.				
			DR	InterPro: IPR003330; SNF2_N.				
			DR	Pfam: PF00271; Helicase_C; 1.				
			DR	Pfam: PF00176; SNP2_N; 1.				
			DR	SMART: SM00487; DEAD_C; 1.				
			DR	SMART: SM00490; HELICC; 1.				
			KW	Complete proteome; Helicase.				
			DR	SEQUENCE 953 AA; 109300 MW; C7C160A9C8105721 CRC64;				
			DR	Best Local Similarity 9.2%; Score 87.5; DB 2; Length 953;				
			DR	Matches 40; Conservative 30; Mismatches 71; Indels 39; Gaps 7;				
			DR	InterPro: IPR0161545; DEAD/DEAH N.				
			DR	InterPro: IPR016150; Helicase_C.				
			DR	InterPro: IPR003330; SNF2_N.				
			DR	Pfam: PF00271; Helicase_C; 1.				
			DR	Pfam: PF00176; SNP2_N; 1.				
			DR	SMART: SM00487; DEAD_C; 1.				
			DR	SMART: SM00490; HELICC; 1.				
			KW	Complete proteome; Helicase.				
			DR	SEQUENCE 953 AA; 109300 MW; C7C160A9C8105721 CRC64;				
			DR	Best Local Similarity 9.2%; Score 87.5; DB 2; Length 953;				
			DR	Matches 40; Conservative 30; Mismatches 71; Indels 39; Gaps 7;				
			DR	InterPro: IPR0161545; DEAD/DEAH N.				
			DR	InterPro: IPR016150; Helicase_C.				
			DR	InterPro: IPR003330; SNF2_N.				
			DR	Pfam: PF00271; Helicase_C; 1.				
			DR	Pfam: PF00176; SNP2_N; 1.				
			DR	SMART: SM00487; DEAD_C; 1.				
			DR	SMART: SM00490; HELICC; 1.				
			KW	Complete proteome; Helicase.				
			DR	SEQUENCE 953 AA; 109300 MW; C7C160A9C8105721 CRC64;				
			DR	Best Local Similarity 9.2%; Score 87.5; DB 2; Length 953;				
			DR	Matches 40; Conservative 30; Mismatches 71; Indels 39; Gaps 7;				
			DR	InterPro: IPR0161545; DEAD/DEAH N.				
			DR	InterPro: IPR016150; Helicase_C.				
			DR	InterPro: IPR003330; SNF2_N.				
			DR	Pfam: PF00271; Helicase_C; 1.				
			DR	Pfam: PF00176; SNP2_N; 1.				
			DR	SMART: SM00487; DEAD_C; 1.				
			DR	SMART: SM00490; HELICC; 1.				
			KW	Complete proteome; Helicase.				
			DR	SEQUENCE 953 AA; 109300 MW; C7C160A9C8105721 CRC64;				
			DR	Best Local Similarity 9.2%; Score 87.5; DB 2; Length 953;				
			DR	Matches 40; Conservative 30; Mismatches 71; Indels 39; Gaps 7;				
			DR	InterPro: IPR0161545; DEAD/DEAH N.				
			DR	InterPro: IPR016150; Helicase_C.				
			DR	InterPro: IPR003330; SNF2_N.				
			DR</td					

Db	113.5	FLEVYERNFHICWDYRFVAAGAAVPPAEEAIFTDSLITRNFSNYSSWHRYSLLPQLHPQ
Qy	111.8	PTAGGRPRGRGL-----
Db	119.5	PDSG-----PQGRLPDVLKELVQNAFFTDDNDQSAFWYHRWL--LGRADPQDALCRLHV
Qy	148.0	---DASVTENFLRLI 159
Db	251.0	SRDZACLTIVFSRPL 265

Search completed: December 29, 2005, 13:59:11
Job time : 230 secs

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OM protein - protein search, using SW model

Run on: December 29, 2005, 13:47:02 ; Search time 38 Seconds
 Post-processing: Minimum Match 0% ; Maximum Match 100%
 (without alignments)
 460.828 Million cell updates/sec

Title: US-10-691-923-34
 Perfect score: 955
 Sequence: 1 MGAVPTSKPTTGKCHIGR.....LKYVADGNLSLRTSTHPEST 182

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% ; Maximum Match 100%
 Listing First 45 summaries

Database : PIR 80.0

1: Pir1;*
 2: Pir2;*
 3: Pir3;*
 4: Pir4;*

Pred. No. is the number of results Predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	83	8.7	567	2 JCS538	Rab geranylgeranyl pre-mRNA splicing protein
2	82	8.6	899	2 S12319	hypothetical protein
3	81.5	8.5	530	2 C75318	HIV-1 retropepsin
4	81.5	8.5	553	1 B46335	probable aldehyde HIV-1 retropepsin
5	81.5	8.5	1086	1	HIV-1 retropepsin
6	80.5	8.4	468	2 T35928	HIV-1 retropepsin
7	80.5	8.4	1101	1 B45390	HIV-1 retropepsin
8	80.5	8.4	1101	1 GNLJVS	B1496_P281 protein
9	79.5	8.3	271	2 S72782	pol protein - Maed
10	79.5	8.3	1087	2 J01162	probable accD3 protein
11	79	8.3	495	2 E07083	hypothetical protein
12	79	8.3	557	2 T4538	high-affinity zinc protein kinase PKN
13	78.5	8.2	253	2 AD0251	hypothetical protein
14	78.5	8.2	942	2 JC2129	beige protein homocysteine efflux system
15	77.5	8.1	217	2 H64186	interferon precursors
16	77.5	8.1	371	2 E72665	benzoylformate dec
17	77.5	8.1	946	2 JC2130	hypothetical protein
18	77	8.1	1035	2 A64686	protein kinase (BC
19	77	8.1	1035	2 T41961	cation efflux system
20	77	8.1	3788	2 T13960	hypothetical protein
21	76.5	8.0	1035	2 D71831	pre-mRNA splicing factor PRP6 - yeast (Saccharomyces cerevisiae)
22	76	8.0	191	2 S57642	N; Alternate names: protein YBR0508; protein YBR05C
23	76	8.0	528	2 C83033	C; Species: Saccharomyces cerevisiae
24	75.5	7.9	403	2 S16603	C; Accession: S12319; S45913; S49510; S55854
25	75.5	7.9	559	2 A83325	R; Legrain, P.; Choulika, A.
26	75.5	7.9	581	2 A81923	EMBO J. 9, 2715-2781, 1990
27	75.5	7.9	649	2 J00103	A; Title: The molecular characterization of PRP6 and PRP9 yeast genes reveals a new cyst
28	75	7.9	654	2 I56134	A; Reference number: S12319; PMID:9036088; PMID:2118103
29	75	7.9	640	1 S37869	

RESULT 1

JCS538

Rab geranylgeranyl transferase (EC 2.5.1.-) alpha chain - human

C;Species: Homo sapiens (man)

C;Date: 01-Sep-1997 #sequence_revision 05-Sep-1997 #text_change 09-Jul-2004

C;Accession: JCS5318

R;Song, H.J.; Rossi, A.; Ceci, R.; Kim, I.G.; Anzano, M.A.; Jang, S.I.; De Laurenzi, V.

Biochem. Biophys. Res. Commun. 235, 10-14, 1997

A;Title: The genes encoding geranylgeranyl transferase alpha-subunit and transglutaminase

A;Reference number: JCS5318; PMID:9196026

A;Molecule type: DNA

A;Residues: 1-567 <SON>

C;Cross-references: UNIPROT:092696; UNIPARC:UPI000013188E

C;Comment: This protein is involved in cutaneous disease.

C;Genetics:

A;Gene: Rabgta

A;Introns: 1/3; 38/3; 81/1; 143/1; 211/1; 238/2; 278/3; 300/3; 336/2; 354/2; 383/2; 413

C;Keywords: transferase

Query Match 8.7%; Score 83; DB 2; Length 567;

Best Local Similarity 25.6%; Pred. No. 7.9; Mismatches 59; Indels 70; Gaps 9;

Matches 50; Conservative 16; MisMatches 59; Indels 70; Gaps 9;

Query 25 SPOELASFKEAR-DALEBSULKKNQNSCSPVPGNWDLRLQYRERPVV-LEAEELALTLK 82

Db 81 SPPESLALVTAELGFLPESCLRV-----NPKSYGTWHRCWMLGRLPPEPNWTRLELCAR 134

Qy 83 VLE-----ARAGPALEDDQPLHTLH-----HILSQLQACIQPQ 117

Db 135 FLEVDERNFICWQDYRERFVATQAAVPAELAFTDDSLITRNFNSYSSWHYRSCLLQLPQ 194

Qy 118 PTAGPRPRGRL-----HHLWHLHQEAQPKESACGL-- 147

Db 195 PDSG-----PQGRLPEDVLLKELELVQNAFFTDNDQSAWYHWRWL-LGRADPQDARCLHV 250

RESULT 2

S12319

pre-mRNA splicing factor PRP6 - yeast (Saccharomyces cerevisiae)

N; Alternate names: protein YBR0508; protein YBR05C

C; Species: Saccharomyces cerevisiae

C; Accession: S12319; S45913; S49510; S55854

R; Legrain, P.; Choulika, A.

EMBO J. 9, 2715-2781, 1990

A; Title: The molecular characterization of PRP6 and PRP9 yeast genes reveals a new cyst

A; Reference number: S12319; PMID:9036088; PMID:2118103

ALIGNMENTS

A;Accession: S12319
 A;Molecule type: DNA
 A;Residues: 1-899 <AL2>
 A;Cross-references: UNIPROT:PI19335; UNIPARC:UPI00000530DB; EMBL:X53465; NID:94218; PID:NID:94218;
 R;Aljinovic, G.; Pohl, F.M.; Pohl, T.M.
 Submitted to the Protein Sequence Database, August 1994
 A;Reference number: S45906
 A;Accession: S45913
 A;Molecule type: DNA
 A;Residues: 1-899 <AL2>
 A;Cross-references: UNIPARC:UPI00000530DB; EMBL:Z35924; NID:9536290; PID:9536291; MIPS:Y
 A;Experimental source: strain S28C
 R;Aljinovic, G.
 Submitted to the EMBL Data Library, October 1994
 A;Description: Sequence and analysis of 24 kb on chromosome II of *Saccharomyces cerevisiae*
 A;Reference number: S49503
 A;Accession: S49510
 A;Molecule type: DNA
 A;Experimental source: strain S28C
 A;Cross-references: UNIPARC:UPI00000530DB; EMBL:Z46260; NID:9559342; PID:9559951
 R;Aljinovic, G.; Pohl, T.M.
 Yeast 11, 475-479, 1995
 A;Title: Sequence and analysis of 24 kb on chromosome II of *Saccharomyces cerevisiae*.
 A;Reference number: S55846; MUID:95321020; PMID:7597852
 A;Accession: S55854
 A;Status: nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-899 <AL2>
 A;Cross-references: UNIPARC:UPI00000530DB; EMBL:Z46260; NID:9559942; PID:CA86398.1; PI
 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1994
 C;Genetics:
 A;Gene: SGD:PRP6
 A;Cross-references: SGD:S0000259; MIPS:YBR055C
 A;Map position: 2R
 C;Keywords: nucleus; RNA binding; zinc finger

Query Match 8.6%; Score 82; DB 2; Length 899;
 Best Local Similarity 22.6%; Pred. No. 17;
 Matches 38; Conservative 27; Mismatches 61; Indels 42; Gaps 8;

Qy 33 RKKARDALEESLKLKNWCSSSPVFPGNWL-DLQLQVRER-----PVA 72
 Db 131 RNKRNRIQEQLNRKTVAAPDSLIPQGNVNDLNKLTTEERKLLQSQIDENLAQLTQKNSNPQ 190

Qy 73 LEAELALT--IKVLEAAGPALEVDLQPLTLHHLISQLOACIQOPTAGPRPRRLHH 130
 Db 191 VNKPNNAITDALSYKDLENDRIVNSLSDATBLQKRTILKSYRKADPT--NPQG---- 243

Qy 131 WL-HRLQEAPKKESA-----GCLB----ASVTFNLFRLTRDVKY 165
 Db 244 WIASARLEEKARKFSVAKKITEENGQCECPRSSDIWLENIRLHESDVYH 291

Matches 44; Conservative 18; Mismatches 68; Indels 25; Gaps 7;
 Qy 25 SPQE-LASFYKKARDALEESLKLKNWCSSSPVFPGNWLRL---LQVPRPVALAEALAL 79
 Db 6 SPSRLRSAGRFIAAPPVGFW-RSPGFGEGSDARLALAHANARRAAALDINM 63

Qy 80 TLKVLEAAAGPALEVDLQPLHTLHHLISL-QACIQOPTAGPRPRGRLLHHLRQEA 138
 Db 64 -----AAGARLEAEVDEQRLPUDQVVERAALVYLFETARRARR----TAAEAA 111

Qy 139 PKKESEAGCLEASVTFNLFRLTRDVKYVADGNL 173
 Db 112 PEATIAADEGARV----QIAKNDVALAYDANL 141

RESULT 4
 C75318 hypothetical protein - *Deinococcus radiodurans* (strain R1)
 C;Species: *Deinococcus radiodurans*
 C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999
 C;Accession: C75318
 R;White, O.; Eisen, J.A.; Heselberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
 M.; Shan, M.; Vahteran, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; M.
 Science 266, 1571-1577, 1999
 A;Title: Genome sequence of the radioresistant bacterium *Deinococcus radiodurans* R1.
 A;Reference number: A75250; MUID:003696; PMID:10567366
 A;Accession: C75318
 A;Species: *Deinococcus radiodurans*
 A;Cross-references: UNIPARC:UPI0000051A67; GB:AE000513; NI:
 A;Experimental source: strain R1
 C;Genetics:
 A;Gene: DR2090
 A;Map position: 1

Query Match 8.5%; Score 81.5; DB 2; Length 553;
 Best Local Similarity 24.0%; Pred. No. 11;
 Matches 40; Conservative 16; Mismatches 64; Indels 47; Gaps 6;

Qy 3 PVPTSKPTTIGRKCHIGRKFLSPLDASPKKARRDABESLKLKWNKSCS-----S 52
 Db 125 PEPKPRPT-----KAAAPYPAASPAETEEAPASAPSGWMSLSSALNDWLKEPEA 174

Qy 53 PVFPGNWLRLQVPRVPALEAHTLKVLEAAGPA-----LIEDV----- 96
 Db 175 PAAPRREAAPARQVRSTATQTQ-----VIAQAPKPAAPQPPDSPLPRTQPEALAS 228

Qy 97 -----DOPLHTLHHLISLQLOACIQOPTAGPRPRGRLLHHLRQEA 139
 Db 229 DRLPDLPVELLERLVEQEQAA-QEQEEPAAPAPVPRVVAALSSAP 274

RESULT 5
 B46335 HIV-1 retropeptin (EC 3.4.23.16) - Maedi/Vienna virus (strain SA-OMVV)
 N;Contains: endonuclease (EC 3.1.1.-); retropeptin (EC 3.4.23.16); RNA-directed DNA pol.
 C;Species: Maedi/Vienna virus
 C;Date: 17-Feb-1994 #sequence_revision 17-Feb-1994
 C;Accession: B46335
 R;Querat, G.; Audoly, G.; Sonigo, P.; Vigne, R.
 Virology 175, 434-447, 1990
 A;Title: Nucleotide sequence analysis of SA-OMVV, a vienna-related ovine lentivirus: phylogenetic analysis
 A;Reference number: A46335; MUID:20223389; PMID:12158181
 A;Accession: B46335
 A;Molecule type: DNA
 A;Residues: 1-1086 <QUE>
 A;Cross-references: UNIPARC:UPI0000131F0D; GB: M31646
 C;Note: This protein is synthesized as a gag-pol polyprotein.
 C;Comment: Specific enzymatic cleavages may yield mature proteins including protease.
 C;Genetics:
 A;Gene: pol

Query Match 8.5%; Score 81.5; DB 2; Length 530;
 Best Local Similarity 28.4%; Pred. No. 10;

C; Superfamily: poi polyprotein
 C; Keywords: AIDS; aspartic proteinase; endonuclease; hydrolase; immunodeficiency; nucleic acid; 20-120/Product: retropepsin #status predicted <RTP>
 P; 129-841/Product: RNA-directed DNA polymerase #status predicted <REV>
 P; 842-1086/Product: endonuclease #status predicted <ENC>
 P; 44/Active site: Asp (shared with dimeric partner) #status predicted

Query Match 8.5%; Score 81.5; DB 1; Length 1086;
 Best Local Similarity 30.0%; Pred. No. 23; Indels 15; Gaps 5;
 Matches 27; Conservative 17; Mismatches 31; Polypeptide: 8.5%
 Qy 3 PVPTRSKPTTGGKCHIGRKFKSLSPQELASFKKARDALESLKL-----KWNSSCSSPVP --- 55
 Db 129 PIRQVKLKEGCKGPHIAQ-PLTQEKLQSLKEVDKLKEKGKVGRAPPHTCNTPIRK 187

Query Match 8.4%; Score 80.5; DB 1; Length 1101;
 Best Local Similarity 31.6%; Pred. No. 30; Indels 15; Gaps 5;
 Matches 25; Conservative 16; Mismatches 23; Polypeptide: 8.4%
 Qy 14 KGCHIGRKFKSLSPQELASFKKARDALESLKL-----KWNSSCSSPVP --- 56
 Db 155 KCPHIAQ-PLTQEKGELKEVDRLEKEGVYGRAPPHTCNTPIRK 213

RESULT 6
 T35928
 probable aldehyde-dehydrogenase - Streptomyces coelicolor
 C; Species: Streptomyces coelicolor
 C; Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
 C; Accession: T35928
 R; Seeger, K.J.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
 Submitted to the EMBL Data Library, January 1999
 A; Reference number: 221551
 A; Accession: AL035206; EMBL:AL035206; PIDN:CAA22750.
 A; Status: preliminary; translated from GB/EMBL/DBJ
 A; Molecular type: DNA
 A; Residues: 1-468 <SEQ>
 A; Cross-references: UNIPROT:Q9ZBH2; UNIPARC:UPI00000DAE91;
 A; Experimental source: strain A1(2)
 C; Genetics:
 A; Gene: SC9DB:SC9BS_08
 C; Superfamily: NAD-dependent aldehyde dehydrogenase; aldehyde dehydrogenase; homology

Query Match 8.4%; Score 80.5; DB 2; Length 468;
 Best Local Similarity 25.7%; Pred. No. 11; Mismatches 16; Polypeptide: 8.4%
 Matches 49; Conservative 16; Mismatches 75; Indels 51; Gaps 10;
 Qy 1 MGPPVPTSKPTTGGKCHIGRKFKSLSPQELASFKKARDALESLKLKWNSSCSSPVP --- 54
 Db 1 MAPATGPRPHTTORG---GYFAVVDPSGEAFAPDRPPEEL-----DPVDRARA 49

Query Match 8.4%; Score 80.5; DB 1; Length 1101;
 Best Local Similarity 31.6%; Pred. No. 30; Indels 15; Gaps 5;
 Matches 25; Conservative 16; Mismatches 23; Polypeptide: 8.4%
 Qy 14 KGCHIGRKFKSLSPQELASFKKARDALESLKL-----KWNSSCSSPVP --- 60
 Db 155 KCPHIAQ-PLTQEKGELKEVDRLEKEGVYGRAPPHTCNTPIRK 213

RESULT 7
 B4 5390 HIV-1 retropepsin (EC 3.4.23.16) - Maedi/Visna virus (strain KV1772) (provirus)
 N; Contains: endonuclease (EC 3.1.-.); retropepsin (EC 3.4.23.16); RNA-directed DNA polymerase
 C; Species: Maedi/Visna virus
 A; Note: host Homo sapiens (man)
 C; Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 03-Jun-2002
 C; Accession: B45390
 R; Andresson, O.S.; Elmer, J.E.; Tobin, G.J.; Greenwood, J.D.; Gonda, M.A.; Georgeson, G.
 J.W.; Petursson, G.
 Virology, 89-105, 1993
 A; Title: Nucleotide sequence and biological properties of a pathogenic proviral molecule
 A; Reference number: A45390; MUID:93174981; PMID:8382414

Submitted to the EMBL Data Library, November 1993
 A; Description: Mycobacterium leprae cosmid B1496.

A; Accession: S72695

A; Status: preliminary

A; Molecule type: DNA

A; Residues: 1-271 <SM1>

A; Cross-references: UNIPROT:Q49706; UNIPARC:UPI00000D4381; EMBL:U00013; NID:9466868; PID:9466868

Query Match 8.3%; Score 79.5; DB 2; Length 271;
 Best Local Similarity 26.2%; Pred. No. 6.9;
 Matches 37; Conservative 24; Mismatches 63; Indels 17; Gaps 7;

Qy 36 RDALEESIQLKKNWCSSSPVPFG--NW-DLRLQ-VRERPVALEAELTLKYLEA--AAG 89

Db 69 RKAELSLKVR ---SAPAMNGKPKDILSKVQWVDPYWPBHTALTVGNLSTNFKTG 124

Qy 90 PALEDVLDQPLHTLHIIHISOLAOACIOPQPTAGPRPRGRLHHLRLOEAPKESAGCLEA 149

Db 125 PAILGADISNHTFTVTDGVER-ETPPLPSP-----HHRPHWGEEGYMPASMGTKEF 177

Qy 150 SYTFNLFRLLTDLKVDAGN 170

Db 178 PTPTGKTYVMSKXDRSVIMDSS 198

RESULT 10
 JQ1162

Pol protein - Maedi/Vienna virus (strain EV1)

C; Species: Maedi/Vienna virus

C; Date: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 09-Jul-2004

C; Accession: JQ1162

R; Sargan, D.R.; Bennet, I.D.; Cousins, C.; Roy, D.J.; Blacklaws, B.A.; Dalziel, R.G.; Wa

J. Gen. Virol. 72, 1873-1903, 1991

A; Title: Nucleotide sequence of EV1, a British isolate of maedi-vienna virus.

A; Reference number: JQ1161; MUID:91341476; PMID:1651983

A; Accession: JQ1162

A; Status: preliminary

A; Molecule type: DNA

A; Residues: 1-1087 <SAR>

A; Cross-references: UNIPROT:Q7L206; UNIPARC:UPI00001785ED

C; Superfamily: pol polyprotein

Query Match 8.3%; Score 79.5; DB 2; Length 1087;

Best Local Similarity 31.6%; Pred. No. 36;

Matches 25; Conservative 16; Mismatches 23; Indels 15; Gaps 5;

Qy 14 KGCHIGRKFISLSPQELASFKGKARDALBESLKL---KWNWCSSPVF----PGNW----D 60

Db 139 KGPHIAW-PLTQEKGLEKIEVERLKEKGKGRAPPHTWCNTPIFCIKKSGKWRMLID 197

Qy 61 LRLLQVRERPVALEELAL 79

Db 198 FRELNKOTELA-EAQQLG 215

RESULT 11
 E70783

probable accD3 protein - Mycobacterium tuberculosis (strain H37RV)

C; Species: Mycobacterium tuberculosis

C; Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004

C; Accession: E70783

R; Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.

i; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.

Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.

Nature 393, 537-544, 1998

A; Authors: Squires, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A; Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome

A; Reference number: A70500; MUID:98395987; PMID:9634230

A; Status: preliminary; nucleic acid sequence not shown; translation not shown

A; Molecule type: DNA

A; Residues: 1-495 <COL>

A; Cross-references: UNIPROT:Q10561; UNIPARC:UPI000001251BA; GB:Z73101; GB:AU123456; NID: A; Experimental source: strain H37RV

C; Genetics: accD3

C; Superfamily: propionyl-CoA carboxylase beta chain

Query Match 8.3%; Score 79; DB 2; Length 495;

Best Local Similarity 28.7%; Pred. No. 16;

Matches 35; Conservative 14; Mismatches 41; Indels 32; Gaps 5;

Qy 64 LQVRPERPVALEAELALTLLKVLBAACPALEVDQD--LHTLHHLSQLQACIOP-----

Db 315 LREARRGMALAAELCPLVLVTDAGCPALSAAEQQGLAGIAHCLAVLVTDLPTVSYL 374

Qy 117 --QPTAGP-----RPRGRHLHHLRLOEAPKESAGCLEAESTVFLNFRLLTDLKYY 166

Db 375 LGQGSGSPALAMLPPADRVLAALHGWLGNPL--PPBEGASA-----IVFRDTAHA 419

Qy 167 AD 168

Db 420 AE 421

RESULT 12
 T24538

hypothetical protein T05F1.1 - Caenorhabditis elegans

C; Species: Caenorhabditis elegans

C; Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

R; Burton, J.

submitted to the EMBL Data Library, November 1996

C; Accession: T24538

R; Sargan, D.R.; Bennet, I.D.; Cousins, C.; Roy, D.J.; Blacklaws, B.A.; Dalziel, R.G.; Wa

J. Gen. Virol. 72, 1873-1903, 1991

A; Title: Nucleotide sequence of EV1, a British isolate of maedi-vienna virus.

A; Reference number: JQ1161; MUID:91341476; PMID:1651983

A; Accession: JQ1162

A; Status: preliminary

A; Molecule type: DNA

A; Residues: 1-1087 <SAR>

A; Cross-references: UNIPROT:Q7L206; UNIPARC:UPI00001785ED

C; Superfamily: Caenorhabditis elegans hypothetical protein T05F1.1

Q; Gene: CESP:T05F1.1

A; Map position: 1

A; Map position: 1/77/2; 119/3; 301/1; 342/2; 536/3

C; Superfamily: Caenorhabditis elegans hypothetical protein T05F1.1

Query Match 8.3%; Score 79; DB 2; Length 557;

Best Local Similarity 19.9%; Pred. No. 18;

Matches 32; Conservative 23; Mismatches 60; Indels 46; Gaps 5;

Qy 20 RFKSLSPQELASFKVKARDALBESLKLKNWCSSPVYFPGNWDLRLQYRERPVALEAL 79

Db 340 RLNSITSP-----KRNIELVTKRKSITVSA-----WEHEKFNKLRMP-----AI 378

Qy 80 TLKVLAAAGPALEVDQD-----LHTLHHLSQLQACIOPQPTAGR-----

Db 379 TLSTLPSPSDPAERNSLDPSALDEDLIDNIRLGEAVLYLIDLPESGPSSSDSRVKSE 438

Qy 124 -----PRGRHLHHLRLOEAPKESAGCLESVTFNL 155

Db 439 ATMLSKDAVDKQRVHIFRQFASRPRVGDRATBTSITSNL 479

RESULT 13
 AD0251

high-affinity zinc uptake system ATP-binding protein [imported] - *Yersinia pestis* (stra

C; Species: *Yersinia pestis*

C; Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 31-Dec-2004

C; Accession: AD0251

R; Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.

deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;

Il, M.; Rutherford, K.; Simmonds, M.; Shelton, J.; Stevens, K.; Whitehead, S.; Barrell,

Nature 413, 523-527, 2001

A; Title: Genome sequence of *Yersinia pestis*, the causative agent of plague.

A; Reference number: AB0001; MUID:21470413; PMID:11586360

A; Accession: Ad0251	Qy 48 WSCSPVPGNWLRLQVRERPVALFELALI-----TLKVLERAAGPALEDVLDQ 98
A; Status: preliminary	Db 407 W---KPCGPNNQDQSPFLERL-ARELELAIVWRDORGLCALKFLK-----LBDFLDN 455
A; Molecule type: DNA	
A; Residues: 1-253 <KUR>	
A; Cross-references: UNIPROT:Q8ZEU3 ; UNIPARC:UPI000000DC6DD ; GB:AL590842 ; PIDN: CAC90872.1;	
C; Genetics:	Qy 99 PHTLHILSOLQACIQOPTAGPRPRGRHLHWRLOEAPKESAGCLEASVTF 153
A; Gene: znuC	Db 456 ERH-----EVOLDMBFO-----GCLVAEYTF 476
Query Match 8.2% ; Score 78.5; DB 2; Length 253;	
Best Local Similarity 28.1%; Pred. No. 7.9;	
Matches 45; Conservative 21; Mismatches 47; Indels 47; Gaps 9;	RESULT 15
Qy 56 PGWDLRLQVRERPVALFELALTLK-----VLEAAAGPALEDV-----LDQPHLT 102	H64186
Db 66 PG---LRGYPEK-LHADATPLTVSREMRLKPGVKADILPLTRQAAHILDQPK 121	hypothetical protein HI1159 - Haemophilus influenzae (strain Rd KW20)
Qy 103 L-----HHLISOLQACIQOPTAGPRGRHLHWRLOEAPKESAGCLEASV 151	C; Species: Haemophilus influenzae
Db 122 LSGGENQRVLLAALLNRPQLLVLDPEQVGVNGOLA-LYDIEQRKE-LGCCAVLMV 178	C; Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004
Qy 152 TFLNLFRLKTRDLYKVAQNLSLR-----TSTHPE 180	C; Accession: H64186
Db 179 SHDULHLYNAK-----TDEVLCLNQHICCSGAPEVVSTHPE 213	A; Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A; Reference number: A64000 ; MUID:95350630 ; PMID:752800	A; Status: nucleic acid sequence not shown; translation not shown
A; Accession: H64186	A; Molecule type: DNA
A; Status: nucleic acid sequence not shown; translation not shown	A; Residues: 1-217 <TIGR>
A; Cross-references: UNIPROT:P43786; UNIPARC:UPI000013A2D0; GB:U32795; NID:91	A; Cross-references: UNIPROT:P43786; UNIPARC:UPI000013A2D0; GB:U32795; NID:91
Query Match 8.1% ; Score 77.5; DB 2; Length 217;	
Best Local Similarity 26.2%; Pred. No. 8.2;	
Matches 45; Conservative 26; Mismatches 66; Indels 35; Gaps 9;	
Qy 9 PRTTGKCHIGFKLSP-QELASFKKARDALEESLKLKNWCSSPVPGNMDRLLQYR 67	
Db 27 PSVLDKSSLIQNLQSLIIPKEEDLFQQLDWFSL---VENYRALPLKQDWFSL---DKK 80	
Qy 68 ERPV-AEABALLTLYKLEAAAGPALEDVLDQ-PLTHLHILSQLQRCIQOPTAGPRPR 125	
Db 81 NSDVALLYAETTYIAKKTEPA---QELINQIPLQDORDSRHGLQAGIELQQQADTPF 135	
Qy 126 GRLHHWLRLQE-----APKESAGCLEASVTPNLFRLITRDL 163	
Db 136 -----IQQLQADYAKNPTAEIAKLVQLHORGNEBEATL-LFGILKTDL 180	
Search completed: December 29, 2005, 13:59:53	
Job time : 40 secs	
A; Cross-references: UNIPROT:Q16512; UNIPARC:UPI000013CB15; GB:D26181; PIDN: R; Palmer, R.H.; Ridder, J.; Parker, P.J.	
Biochem. Biophys. Res. Commun. 199, 897-904, 1994	
A; Title: A novel protein kinase with zipper-like sequences: Its catalytic domain	
A; Reference number: JG2129; MUID:94183274 ; PMID:8135837	
A; Accession: JC2129	
A; Molecule type: mRNA	
A; Residues: 1-942 <MDR>	
A; Cross-references: UNIPROT:Q16512; UNIPARC:UPI000013CB15; GB:D26181; PIDN: R; Palmer, R.H.; Ridder, J.; Parker, P.J.	
Biochem. Biophys. Res. Commun. 199, 897-904, 1994	
A; Title: A novel protein kinase with zipper-like sequences: Its catalytic domain	
A; Reference number: JG2129; MUID:94183274 ; PMID:8135837	
A; Accession: S67526	
A; Molecule type: mRNA	
A; Residues: 1-190, 'D'192-942 <PAL>	
A; Cross-references: UNIPARC:UPI0000131B6B; EMBL:S75546; NID:9314097; PIDN: AAB33345.1; PI	
A; Experimental source: fetal brain	
R; Palmer, R.H.; Ridder, J.; Parker, P.J.	
FEBS Lett. 356, 5-8, 1994	
A; Title: Identification of multiple, novel, protein kinase C-related gene products.	
A; Reference number: S51020 ; PMID:7988719	
A; Accession: S51020	
A; Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra	
A; Molecule type: mRNA	
A; Residues: 700-799, 'A' <PA2>	
A; Cross-references: UNIPARC:UPI000017A3BB	
C; Comment: This protein has a protein kinase domain related to protein kinase C.	
C; Keywords: ATP; leucine zipper; phosphotransferase; protein kinase	
F; 39-56/Region: basic	
F; 70-287/Region: leucine zipper motif	
F; 613-874/Region: protein kinase homology <KIN>	
F; 621-629/Region: protein kinase ATP-binding motif	
F; 644/Active site: Lys #status predicted	
Query Match 8.2% ; Score 78.5; DB 2; Length 942;	
Best Local Similarity 28.6%; Pred. No. 38;	
Matches 50; Conservative 14; Mismatches 40; Indels 71; Gaps 13;	
Qy 2 GP-VPTSKP---TTTGKCHIGFKLSPQELASFKKARDALEESLKLKN-----47	
Db 350 GPCTPDSSRPPFLSRPARGLY-SRSGSLSGR--SSLKAEAENTSEVSTVLLKLDNTVVGTS 406	

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 29, 2005, 13:29:22 (without alignments)

427,631 Million cell updates/sec
Perfect score: 955
Sequence: 1 MGPPVPTSKPTTGTGCHIGR.....LKVADGNLSSLRTSTHPBST 182

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 4393781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq 21:
1: geneseqP19908:/*
2: geneseqP19908:/*
3: geneseqP20018:/*
4: geneseqP20018:/*
5: geneseqP20018:/*
6: geneseqP2003as:/*
7: geneseqP2003as:/*
8: geneseqP20048:/*
9: geneseqP20058:/*

Score: No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	955	100.0	182	8	AD059974		Ado59974 Met IL-28
2	955	100.0	182	9	ADY03602		Ady03602 Human IL-28
3	951	99.6	182	9	ADY03614		Ady03614 Human IL-28
4	950	99.5	181	9	AD059972		Ado59972 IL-28A mu
5	950	99.5	181	9	ADY03600		Ady03600 Human IL-28
6	950	99.5	182	8	AD059978		Ado59978 Met IL-29
7	950	99.5	182	9	ADY03588		Ady03588 Human IL-29
8	948	99.3	183	9	ADY03724		Ady03724 Human IL-29
9	947	99.2	183	9	ADY03728		Ady03728 Human IL-29
10	946	99.1	181	9	ADY03613		Ady03613 Human IL-29
11	946	99.1	182	9	ADY03658		Ady03658 Human IL-29
12	946	99.1	185	9	ADY03734		Ady03734 Human IL-29
13	945	99.0	182	9	ADY03662		Ady03662 Human IL-29
14	945	99.0	200	5	AAB18311		Aab18311 Human ZCY
15	945	99.0	200	5	AAB18310		Aab18310 Human ZCY
16	945	99.0	200	8	AD059960		Ado59960 IL-29. 7/
17	945	99.0	200	9	ADY03577		Ady03577 Human IL-29
18	944	98.8	182	9	ADY03678		Ady03678 Human IL-29
19	946	98.5	181	9	ADY03656		Ady03656 Human IL-29
20	941	98.5	182	9	ADY03730		Ady03730 Human IL-29
21	941	98.5	182	9	ADY03726		Ady03726 Human IL-29
22	940	98.4	180	9	ADY03712		Ady03712 Human IL-29
23	940	98.4	181	9	ADY03660		Ady03660 Human IL-29
24	940	98.4	182	9	ADY03670		Ady03670 Human IL-29

ALIGNMENTS

RESULT 1

ADO59974

ID AD059974 standard; protein; 182 AA.

XX

AC ADO59974;

XX

DT 29-JUL-2004 (first entry)

XX

DB Met IL-28A mutant C172S.

XX

KW interleukin; IL-28A; viral; infection; liver; inflammation;

KW viral load; anti-viral antibody; serological level;

KW alanine aminotransferase; histological improvement; hepatitis B;

KW hepatitis C; cytopenia; leucocyte deficiency; neutropenia;

KW thrombocytopenia; anaemia; IL-29.

XX

OS Homo sapiens.

XX

PH key

FT misc-difference 172

XX

/label= C172S

SUMMARIES

WO2004037995-A2.

PN

PN

PD

XX

Treating hepatitis B or hepatitis C virus infection comprises administering to a mammal with viral infection causing liver inflammation, a polypeptide that is conjugated to a polyalkyl oxide group.

Claim 12; SEQ ID NO 34; 102pp; English.

CC This sequence represents a mutant interleukin 1L-28A, Met-C172S. This
 CC interleukin protein may be used in the method of the invention for
 CC treating a viral infection. The method comprises administering to a
 CC mammal with a viral infection causing liver inflammation, an interleukin-
 CC based polypeptide, where the viral infection level or liver inflammation
 CC is reduced. The reduction in the viral infection level is measured as a
 CC decrease in viral load, an increase in anti-viral antibodies, a decrease
 CC in serological levels of alanine aminotransferase or histological
 CC improvement. The viral infection is hepatitis B or C virus infection. The
 CC mammal has cytopenia, comprising leukocyte deficiency, neutropenia,
 CC thrombocytopenia or anaemia. The interleukin polypeptide is interleukin
 CC 28 or 29, or a variant of these. The method of the invention is useful in
 CC treating hepatitis B or C virus infection.

XX Sequence 182 AA;

Query Match Score 955; DB 8; Length 182;

Best Local Similarity 100.0%; Pred. No. 2.8e-91;

Matches 182; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MGPPVPTSKPTTRNGKGCIGRKFSLSPOLASKKARDALEESLKLXNWCSSPVFGNWD 60

Db 1 MGPPVPTSKPTTRGKGCIGRKFSLSPOLASKKARDALEESLKLXNWCSSPVFGNWD 60

Qy 1 LRLLQYRERPVALEELAATLKVLEAGPALEVDLQPLHTLHILSOLACIQOPTA 120

Db 1 LRLLQYRERPVALEELAATLKVLEAGPALEVDLQPLHTLHILSOLACIQOPTA 120

Qy 121 GPRPRGLHLWHLRQAPKESAGCLEASVTFNLFLRLDKYVADGNLSLRSTHPE 180

Db 121 GPRPRGLHLWHLRQAPKESAGCLEASVTFNLFLRLDKYVADGNLSLRSTHPE 180

Qy 181 ST 182

Db 181 ST 182

RESULT 2
ADY03602 standard; protein; 182 AA.

XX ADY03602;

XX 05-MAY-2005 (first entry)

XX Human IL-29 mutant protein sequence SeqID29.

XX antiviral; pharmaceutical; hepatitis b virus infection;

XX hepatitis c virus infection; mutant; mutein; IL-29.

XX Homo sapiens.

OS Synthetic.

XX US2005037012-A1.

XX PD 17-FEB-2005.

XX PF 09-AUG-2004; 2004US-00914772.

XX PR 07-AUG-2003; 2003US-0493194P.

PR 10-MAR-2004; 2004US-055181P.

PR 02-APR-2004; 2004US-055914P.

XX (BRAD/) BRADY L J.

PA (KLUC/) KLUCHER K M.

PA (CHAN/) CHAN C.

PA (DONG/) DONG D L.

PA (LIU/) LIU H Y.

PA (SHEP/) SHEPPARD P O.

PA (BUKOWSKI/) BUKOWSKI T R.

PI Brady LJ, Klucher KM, Chan C, Dong DL, Liu HY, Sheppard PO,

PI PI PI PI

XX WPI; 2005-180368/19.
 DR N-PDB; ADY03601.

XX Novel isolated Interleukin-28A, IL-28B or IL-29 polypeptide having anti-viral activity, useful for treating hepatitis B or hepatitis C infections.

XX Claim 1; SEQ ID NO 29; 149pp; English.

XX This invention relates to a novel isolated IL-28A, IL-28B or IL-29 polypeptide having antiviral activity. One or more of the cysteine residues were mutated to produce the proteins of the invention. The invention may be useful for the development of a pharmaceutical composition for the treatment of hepatitis B or C. The present sequence is that of a novel IL variant protein of the invention.

XX SQ Sequence 182 AA;

Query Match Score 955; DB 9; Length 182;

Best Local Similarity 100.0%; Pred. No. 2.8e-91;

Matches 182; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGPPVPTSKPTTRNGKGCIGRKFSLSPOLASKKARDALEESLKLXNWCSSPVFGNWD 60

Db 1 MGPPVPTSKPTTRGKGCIGRKFSLSPOLASKKARDALEESLKLXNWCSSPVFGNWD 60

Qy 1 MGPPVPTSKPTTRGKGCIGRKFSLSPOLASKKARDALEESLKLXNWCSSPVFGNWD 60

Db 1 MGPPVPTSKPTTRGKGCIGRKFSLSPOL

XX	09-AUG-2004;	2004US-00914772.	OS	Homo sapiens.
XX			XX	WO2004037995-A2.
PR	07-AUG-2003;	2003US-0493194P.	PN	
PR	10-MAR-2004;	2004US-0551641P.	XX	
PR	02-APR-2004;	2004US-0559142P.	PD	06-MAY-2004.
XX			XX	
(BRAD/)	BRADY L J.		XX	23-OCT-2003;
PA	(KLUC/)	KLUCHER K M.	PF	2003WO-US033628.
PA	(CHAN/)	CHAN C. C.	XX	
PA	(DONG/)	DONG D L.	PR	23-OCT-2002;
PA	(LIUD/)	LIU H Y.	PR	2002US-0420713P.
PA	(SHEP/)	SHEPPARD P O.	PR	18-APR-2003;
PA	(BUKO/)	BUKOWSKI T R.	PR	2003US-0463982P.
XX			XX	
PI	Brady LJ,	Klucher KM,	PA	(ZYMO) ZYMOGENETICS INC.
PI	Chan C,	Dong DL,	PA	
PI	Liu HY,	Sheppard PO;	PA	
PI	Bukowski TR;		XX	
XX			XX	
DR	WPI: 2005-180368/19.		WPI: 2004-365507/34.	
DR	N-PSDB;	AD035977.	DR	
XX			XX	
XX	Novel isolated Interleukin-28A, IL-28B or IL-29 polypeptide having anti-viral activity, useful for treating hepatitis B or hepatitis C infections.		PT	Treating hepatitis B or hepatitis C virus infection comprises administering to a mammal with a viral infection causing liver inflammation, a polypeptide that is conjugated to a polyalkyl oxide group.
PT			PT	
PT			PT	
XX			XX	
PS	PS ID NO 27;	149pp;	English.	Claim 13; SEQ ID NO 38; 102PP; English.
XX			XX	
CC	This invention relates to a novel isolated IL-28A, IL-28B or IL-29 polypeptide having antiviral activity. One or more of the cysteine residues were mutated to produce the proteins of the invention. The invention may be useful for the development of a pharmaceutical composition for the treatment of hepatitis B or C. The present sequence is that of a novel IL variant protein of the invention.		CC	This sequence represents an interleukin Met-IL-29. This interleukin protein may be used in the method of the invention for treating a viral infection. The method comprises administering to a mammal with a viral infection causing liver inflammation, an interleukin-based polypeptide, where the viral infection level or liver inflammation is reduced. The reduction in the viral infection level is measured as decrease in viral load, an increase in anti-viral antibodies, a decrease in serological levels of alanine aminotransferase or histological improvement. The viral infection is hepatitis B or C virus infection. The mammal has cytopaenia, comprising leukocyte deficiency, neutropenia, thrombocytopenia or anaemia. The interleukin polypeptide is interleukin 28 or 29, or a variant of these. The method of the invention is useful in treating hepatitis B or C virus infection.
XX			CC	
SQ	Sequence 181 AA;		XX	Sequence 182 AA;
Query	2 GPVPTSKPTTGKGCHIGRKFKSLSPQELASPKKARDALEEBSLKLKNWCSSSPVFPGNWDL	99.5%;	Query Match	99.5%;
Best Local Similarity	100.0%;	Score 950;	Best Local Similarity	99.5%;
Matches	181;	DB 9;	Matches	0;
Db	1 GPVPTSKPTTGKGCHIGRKFKSLSPQELASPKKARDALEEBSLKLKNWCSSSPVFPGNWDL	Length 181;	DB 8;	Score 950;
Qy	62 RLLQVRERPVALEELALTIVKLEAAAGPALEVDLQPLHILHLSQLOACIQQOPTAG	Length 181;	DB 8;	Length 182;
Db	61 RLLQVRERPVALEELALTIVKLEAAAGPALEVDLQPLHILHLSQLOACIQQOPTAG	120	Qy	1 MGVPVTSKPTTGKGCHIGRKFKSLSPQELASPKKARDALEEBSLKLKNWCSSSPVFPGNWDL 60
Qy	122 PRPRGRGLHHWLRQELQPKRSAGCKEASVTFNLFRLLTRDLYVADGNLSLRTSTHPE	181	Db	1 MGVPVTSKPTTGKGCHIGRKFKSLSPQELASPKKARDALEEBSLKLKNWCSSSPVFPGNWDL 60
Db	121 PRPRGRGLHHWLRQELQPKRSAGCKEASVTFNLFRLLTRDLYVADGNLSLRTSTHPE	180	Qy	61 LRLQVRERPVALEELALTIVKLEAAAGPALEVDLQPLHILHLSQLOACIQQOPTA 120
Qy	182 T 182		Db	61 LRLQVRERPVALEELALTIVKLEAAAGPALEVDLQPLHILHLSQLOACIQQOPTA 120
Db	181 T 181		Qy	121 GPRPRGRGLHHWLRQELQPKRSAGCKEASVTFNLFRLLTRDLYVADGNLSLRTSTHPE 180
RESUIT 6			Db	121 GPRPRGRGLHHWLRQELQPKRSAGCKEASVTFNLFRLLTRDLYVADGNLSLRTSTHPE 180
ADD039978	ID ADD05978 standard;	protein; 182 AA.	Qy	181 ST 182
XX	AC ADD05978;		Db	181 ST 182
XX	DT 29-JUL-2004 (first entry)		RESULT 7	ADY03588
DB	Met IL-29.		ID	ADY03588 standard; protein; 182 AA.
XX	interleukin; IL-28A; IL-28B; viral; infection; liver; inflammation;		XX	
XX	viral load; anti-viral antibody; serological level;		AC	ADY03588;
XX	alanine aminotransferase; histological improvement; hepatitis B;		XX	
XX	hepatitis C; cytopaenia; neutropenia; thrombocytopenia;		DT	05-MAY-2005 (first entry)
XX	anaemia; IL-29.		XX	Human IL-29 mutant protein sequence SeqID15
DE			DE	

RESULT 10

AC ADY03728; XX
 DT 05-MAY-2005 (first entry) XX
 DE Human IL-29 mutant protein sequence SeqID155. XX
 XX antiviral; pharmaceutical; hepatitis b virus infection; XX
 KW hepatitis c virus infection; mutant; mutein; IL-29. XX
 XX OS Homo sapiens. XX
 OS Synthetic. XX
 PN US2005037012-A1. XX
 XX PD 17-FEB-2005. XX
 XX PF 09-AUG-2004; 2004US-00914772. XX
 XX PR 07-AUG-2003; 2003US-0493124P. XX
 PR 10-MAR-2004; 2004US-055181P. XX
 PR 02-APR-2004; 2004US-0559142P. XX
 XX (BRAD/) BRADY L J. PA
 PA (KLUC/) KLucher K M. PA
 PA (CHAN/) CHAN C. PA
 PA (DONG/) DONG D L. PA
 PA (LIUH/) LIU H Y. PA
 PA (SHEPPARD/) SHEPPARD P O. PA
 PA (BUKO/) BUKOWSKI T R. PA
 PI Brady LJ, Klucher KM, Chan C, Dong DL, Liu HY, Sheppard PO; PI
 PI BUKOWSKI TR; PI
 DR WPI; 2005-180368/19. PI
 DR N-PSDB; ADY03727. PI
 XX PT Novel isolated Interleukin-28A, IL-28B or IL-29 polypeptide having anti-viral activity, useful for treating hepatitis B or hepatitis C PT
 PT Novel isolated Interleukin-28A, IL-28B or IL-29 polypeptide having anti-viral activity, useful for treating hepatitis B or hepatitis C PT
 XX PS Claim 1; SEQ ID NO 155; 149pp; English. PT
 XX This invention relates to a novel isolated IL-28A, IL-28B or IL-29 polypeptide having antiviral activity. One or more of the cysteine residues were mutated to produce the proteins of the invention. The invention may be useful for the development of a pharmaceutical composition for the treatment of hepatitis B or C. The present sequence is that of a novel IL variant protein of the invention. PT
 XX SQ Sequence 183 AA; PT
 XX Query Match 99.2%; Score 947; DB 9; Length 183; PT
 Best Local Similarity 98.9%; Pred. No. 1.9e-90; PT
 Matches 180; Conservative 1; Mismatches 1; Indels 0; Gaps 0; PT
 PT
 Qy 1 MGPVPTSKPTTGKCHIGRKFLSPQELASPKARDALEESLKLKWNSCSPVFGNWD 60 PT
 Db 2 1GPVPTSKPTTGKCHIGRKFLSPQELASPKARDALEESLKLKWNSCSPVFGNWD 61 PT
 Qy 61 LRLLQVRERPVALEELATLKVLEAGPALEDVLDQPLTLHHLISQLOACIQOPTA 120 PT
 Db 62 LRLLQVRERPVALEELATLKVLEAGPALEDVLDQPLTLHHLISQLOACIQOPTA 121 PT
 Qy 121 GPRPRGRHLHMLQAPKKESSAGCLEASVTFNLFRLTRDLKTYADGNLSLRTSHP 180 PT
 Db 122 GPRPRGRHLHMLQAPKKESSAGCLEASVTFNLFRLTRDLKTYADGNLXLRTSHP 181 PT
 Qy 181 ST 182 PT
 Db 182 ST 183 PT
 Qy 182 T 182 PT

Db	181 T 181	Qy	181 ST 182
RESULT 11			
ID ADY03658	Human IL-29 mutant protein sequence SeqID85.	Db	181 ST 182
ID ADY03658 standard; protein, 182 AA.			
AC ADY03658;			
XX 05-MAY-2005 (first entry)			
XX DE Human IL-29 mutant protein sequence SeqID85.			
XX KW antiviral; pharmaceutical; hepatitis b virus infection;			
XX KW hepatitis c virus infection; mutant; mutein; IL-29.			
XX OS Homo sapiens.			
XX OS Synthetic.			
PN US2005037012-A1.			
XX PD 17-FEB-2005.			
XX PP 09-AUG-2004; 2004US-00914772.			
PR 07-AUG-2003; 2003US-0493194P.			
PR 10-MAR-2004; 2004US-0551841P.			
PR 02-APR-2004; 2004US-0559142P.			
XX PA (BRAD/.) BRADY L J.			
PA (KLUC/.) KLUCHER K M.			
PA (CHAN/.) CHAN C.			
PA (DONG/.) DONG D L.			
PA (LIU/.) LIU H Y.			
PA (SHEP/.) SHEPPARD P O.			
PA (BUKO/.) BUKOWSKI T R.			
PI Brady LJ, Klucher KM, Chan C, Dong DL, Liu HY, Sheppard PO;			
PI Bukowski TR;			
DR WPI: 2005-180368/19.			
DR N-PSDB; ADY03657.			
PT Novel isolated Interleukin-28A, IL-28B or IL-29 polypeptide having anti-viral activity, useful for treating hepatitis B or hepatitis C			
PT Novel isolated Interleukin-28A, IL-28B or IL-29 polypeptide having anti-viral activity, useful for treating hepatitis B or hepatitis C			
PT Novel isolated Interleukin-28A, IL-28B or IL-29 polypeptide having anti-viral activity, useful for treating hepatitis B or hepatitis C			
PT Novel isolated Interleukin-28A, IL-28B or IL-29 polypeptide having anti-viral activity, useful for treating hepatitis B or hepatitis C			
PS Claim 1; SEQ ID NO 85; 149pp; English.			
CC This invention relates to a novel isolated IL-28A, IL-28B or IL-29 polypeptide having antiviral activity. One or more of the cysteine residues were mutated to produce the proteins of the invention. The invention may be useful for the development of a pharmaceutical composition for the treatment of hepatitis B or C. The present sequence is that of a novel IL variant protein of the invention.			
XX Sequence 182 AA;			
XX Query Match 99.1%; Score 946; DB 9; Length 182;			
XX Best Local Similarity 98.9%; Pred. No. 2.4e-90; Indels 0; Gaps 0;			
XX Matches 180; Conservative 1; Mismatches 1; Gaps 0;			
Qy 1 MGPPVPSKPTTGGCHIGRKFKSLSPQELASFKKKARDALBESLKLKWNWCSSSPVPPGNWD	Query Match 99.1%; Score 946; DB 9; Length 185;		
Qy 1 MGPPVPSKPTTGGCHIGRKFKSLSPQELASFKKKARDALBESLKLKWNWCSSSPVPPGNWD	Best Local Similarity 99.4%; Pred. No. 2.5e-90; Indels 0; Gaps 0;		
Db 1 LRLQVRERPVVALEALTLKVLEAAGPALEVDLQPLTLHHLSQLACIQOPTA	Matches 180; Conservative 0; Mismatches 1; Gaps 0;		
Qy 61 LRLQVRERPVVALEALTLKVLEAAGPALEVDLQPLTLHHLSQLACIQOPTA	Qy 2 GPVPSSKPTTGGCHIGRKFKSLSPQELASFKKKARDALBESLKLKWNWCSSSPVPPGNWD	61	
Db 61 LRLQVRERPVVALEALTLKVLEAAGPALEVDLQPLTLHHLSQLACIQOPTA	Db 5 GPVPSSKPTTGGCHIGRKFKSLSPQELASFKKKARDALBESLKLKWNWCSSSPVPPGNWD	64	
Qy 121 GPRPRGRLLHHLRLQEAPKKESAGCLESYTFENLFRLLTRDLKYADGNLSLRTSTHPE	Qy 62 RLLQVRERPVVALEALTLKVLEAAGPALEVDLQPLTLHHLSQLACIQOPTAG	121	
Db 121 GPRPRGRLLHHLRLQEAPKKESAGCLESYTFENLFRLLTRDLKYADGNLSLRTSTHPE	Db 65 RLLQVRERPVVALEALTLKVLEAAGPALEVDLQPLTLHHLSQLACIQOPTAG	124	

Qy	122	PRPRGLHLHHLRQEAQKESAGCLEASVTFNLFLLTRDLYVADGNLSLRSTHPE	181	Db	61	LRLLQYRERPVALEAELAATLKVLEAAAGPALEDVLDQPLHTLHILSOLQACIQPQPTA	120
Db	125	PRPRGLHLHHLRQEAQKESAGCLEASVTFNLFLLTRDLYVADGNXLRTSTHPE	184	Qy	121	GPRPGRLHLRQEAQKESAGCLEASVTNFILRLTRDLYVADGNLSLRSTHPE	180
Qy	182	T 182		Db	121	GPRPGRLHLRQEAQKESAGCLEASVTNFILRLTRDLYVADGNXLRTSTHPE	180
Db	185	T 185		Qy	181	ST 182	
RESULT 13				Db	181	ST 182	
ADY03662				RESULT 14			
ID	ADY03662	standard; protein: 182 AA.		ID	AAE18311	standard; protein: 200 AA.	
XX	AC	ADY03662;		ID	AAE18311;		
XX	DT	05-MAY-2005 (first entry)		ID	AAE18311;		
XX	DE	Human IL-29 mutant protein sequence SeqID89.		XX			
XX	XX	antiviral; pharmaceutical; hepatitis b virus infection; hepatitis c virus infection; mutant; murine; IL-29.		DT	07-MAY-2002 (first entry)		
KW	XX			XX			
KW	XX	Human; interferon like protein; IFN; genetic disease; transgenic animal; cancer; immune regulation; rheumatoid arthritis; multiple sclerosis; myasthenia gravis; systemic lupus erythematosus; diabetes; inflammation; tumour; viral infection; graft rejection; human immuno deficiency virus; HIV; behavioural disorder; reproductive disorder; vaccine adjuvant; sepsis; cytostatic; neuroprotective; dermatological; immunosuppressive; zcyt21 protein; chromosome 19q13.13.		XX			
XX	XX			DE	Human Zcyt21 consensus protein.		
OS	XX			XX			
OS	OS			KW			
Synthetic.	Synthetic.			KW			
XX	XX			KW			
US2005037012-A1.	US2005037012-A1.			KW			
XX	XX			KW			
PD	17-FEB-2005.			KW			
XX	XX			KW			
PF	09-AUG-2004; 2004US-00914772.			KW			
XX	XX			KW			
PF	07-AUG-2003; 2003US-0493194P.			KW			
PR	10-MAR-2004; 2004US-0551941P.			KW			
PR	02-APR-2004; 2004US-0559142P.			KW			
XX	XX			KW			
PA	(BRAD/)	BRADY L J.		KW			
PA	(KLJIC/)	KLUCHER K M.		KW			
PA	(CHAN/)	CHAN C.		KW			
PA	(DONG/)	DONG D L.		KW			
PA	(LITCH/)	LIU H Y.		KW			
PA	(SHEPP/)	SHEPPARD P O.		KW			
PA	(BURO/)	BUKOWSKI T R.		KW			
XX	XX			KW			
Brady LJ., Klucher KM., Chan C., Dong DL., Liu HY., Sheppard PO., Bukowski TR;	PI	Sheppard PO, Presnell SR, Fox BA, Gilbert T, Haldeman BA;		KW			
XX	XX			KW			
WPI; 2005-180368/19.	PI	Grant FU;		KW			
DR	DR	WPI; 2002-171540/22.		KW			
N-PSDB; ADY03661.	DR	N-PSDB; AAD29446.		KW			
XX	XX			KW			
PT	Novel isolated Interleukin-28A, IL-28B or IL-29 polypeptide having anti-viral activity, useful for treating hepatitis B or hepatitis C infections.	PT	New polypeptide Zcyt21, which is related to interferon, is useful e.g. for treating viral infection and immunological disease.	PT			
PT	Novel isolated Interleukin-28A, IL-28B or IL-29 polypeptide having anti-viral activity, useful for treating hepatitis B or hepatitis C infections.	PT	New polypeptide Zcyt21, which is related to interferon, is useful e.g. for treating viral infection and immunological disease.	PT			
XX	XX			XX			
XX	XX			PS	Disclosure; Page 75; 82pp; English.		
PS	PS			XX			
PS	PS			CC	The patent discloses novel polynucleotide and polypeptide molecules for		
PS	PS			CC	Zcyt21, an interferon (IFN) like protein which is most closely related		
PS	PS			CC	to INF-alpha. Zcyt21 DNAs are useful for detecting the corresponding		
PS	PS			CC	genes and its mutants, e.g. for diagnosis of genetic diseases and cancer		
PS	PS			CC	or for detecting chromosome 19 deletions and translocations associated		
PS	PS			CC	with diseases. They are useful for preparing transgenic animals used to		
PS	PS			CC	study the Zcyt21 gene and protein and as antisense inhibitors. Zcyt21		
PS	PS			CC	sequences and their inhibitors are useful for treating diseases that		
PS	PS			CC	require immune regulation (e.g. rheumatoid arthritis, multiple sclerosis,		
PS	PS			CC	myasthenia Gravis, systemic lupus erythematosus and diabetes), tumours,		
PS	PS			CC	inflammation (e.g. arthritis or sepsis), viral infections (e.g. human		
PS	PS			CC	immune deficiency viruses (HIV) and papilloma viruses), graft rejection,		
PS	PS			CC	behavioural and reproductive disorders. They are also used as vaccine		
PS	PS			CC	adjuvants. They can also be used to identify specific inhibitors and		
PS	PS			CC	receptors. The present sequence is human Zcyt21 consensus protein.		
PS	PS			CC	Zcyt21 gene is located on chromosome 19q13.13		
PS	PS			XX	Sequence 200 AA;		
Query Match	99.0%	Score 945; DB 9;	Length 182;	XX			
Best Local Similarity	98.9%	Pred. No. 3.1e-90;		XX			
Matches 180;	Conservative 0;	Mismatches 0;	Indels 0;	XX			
Qy	1 MGPPVPTSKPTPGKFGHIGRKFLSPOELASPKARDALLESLKLXKNWSSSPVFGNWD 60			XX			
Db	1 MGPPVPTSKPTPGKFGHIGRKFLSPOELASPKARDALLESLKLXKNWSSSPVFGNWD 60			XX			
Qy	61 LRLLQYRERPVALEAELAATLKVLEAAAGPALEDVLDQPLHTLHILSOLQACIQPQPTA 120			SQ			

Query Match 99.0%; Score 945; DB 5; Length 200;
 Best Local Similarity 99.4%; Pred. No. 3.5e-90;
 Matches 180; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 CC inflammation (e.g., arthritis or sepsis), viral infections (e.g., human
 immune deficiency viruses (HIV) and papilloma viruses), graft rejection,
 behavioural and reproductive disorders. They are also used as vaccine
 CC adjuvants. They can also be used to identify specific inhibitors and
 CC receptors. The present sequence is human zcyt21 allelic variant protein
 XX

Qy 2 GPVPTSKPTTGGCKGCHIGRKFSLSKPOELASFKKARDALBESLKLKWNSSSPVPGNWL 61
 Db 20 GPVPTSKPTTGGCKGCHIGRKFSLSKPOELASFKKARDALBESLKLKWNSSSPVPGNWL 79
 SQ Sequence 200 AA;

Query Match 99.0%; Score 945; DB 5; Length 200;
 Best Local Similarity 99.4%; Pred. No. 3.5e-90;
 Matches 180; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 CC

Qy 62 RLLQYRERPVALEALTLKVLAAAGPALEVDQPLHTLHILSQACIOQPTAG 121
 Db 80 RLLQYRERPVALEALTLKVLAAAGPALEVDQPLHTLHILSQACIOQPTAG 139
 CC

Qy 122 PRPRGLRHLHRLQEAPEKKSAGLEASVTNPLRLKVAADGNLISLRSTHPPS 181
 Db 140 PRPRGLRHLHRLQEAPEKKSAGLEASVTNPLRLKVAADGNLISLRSTHPPS 199
 CC

Qy 182 T 182
 Db 200 T 200
 CC

Db 140 PRPRGLRHLHRLQEAPEKKSAGLEASVTNPLRLKVAADGNLISLRSTHPPS 199
 CC

RESULT 15
 AAE18310
 ID AAE18310 standard; protein; 200 AA.
 XX
 AC AAE18310
 AC
 AC 182 T 182
 AC
 AC 200 T 200
 CC

DT 07-MAY-2002 (first entry)
 XX
 DE Human zcyt21 allelic variant protein.
 XX
 Human; interferon like protein; IFN; genetic disease; transgenic animal;
 KW cancer; immune regulation; rheumatoid arthritis; multiple sclerosis;
 KW myasthenia gravis; systemic lupus erythematosus; diabetes; inflammation;
 KW tumour; viral infection; graft rejection; human immuno deficiency virus;
 KW HIV; behavioural disorder; reproductive disorder; vaccine adjuvant;
 KW sepsis; cytostatic; neuroprotective; dermatological; immunosuppressive;
 KW zcyt21 protein.
 XX
 OS Homo sapiens.
 PN WO200202627-A2.
 XX
 PD 10-JAN-2002.
 XX
 PF 29-JUN-2001; 2001WO-US021087.
 XX
 PR 30-JUN-2000; 2000US-0215446P.
 PR 20-APR-2001; 2001US-0285424P.
 XX
 PA (ZYMO) ZYMOGENETICS INC.
 XX
 Sheppard PO, Preneell SR, Fox BA, Gilbert T, Haldeman BA;
 PI Grant PJ;
 XX
 DR WPI; 2002-171640/22.
 DR N-PSBB; AAD29145.
 PT
 PT
 Disclosure: Page 72-73; 82pp; English.
 PS

XX The patent discloses novel polynucleotide and polypeptide molecules for
 CC zcyt21, an interferon (IFN) like protein that is most closely related
 CC to INF-alpha. Zcyt21 DNAs are useful for detecting the corresponding
 CC genes and its mutants, e.g. for diagnosis of genetic diseases and cancer
 CC or for detecting chromosome 19 deletions and translocations associated
 CC with disease. They are useful for preparing transgenic animals used to
 CC study the zcyt21 gene and protein and as antisense inhibitors. Zcyt21
 CC sequences and their inhibitors are useful for treating diseases that
 CC require immune regulation (e.g. rheumatoid arthritis, multiple sclerosis,
 CC myasthenia gravis, systemic lupus erythematosus and diabetes), tumours,

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OM protein - protein search, using SW model

Run on: December 29, 2005, 13:47:27 ; Search time 46 seconds

327,108 Million cell updates/sec
(without alignments)

Title: US-10-691-923-34

Perfect score: 955

Sequence: 1 MGPPVPTSKPTTGGCHIGR.....LKTVADGNLSLRTSTHPEST 182

Scoring table: BLOSUM62

Gapopen 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing First 45 summaries

Database : Issued Patents AA:*

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3: /gn2_6/ptodata/1/iaa/11_COMB.pep:*

4: /gn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

5: /gn2_6/ptodata/1/iaa/RE_COMB.pep:*

6: /gn2_6/ptodata/1/iaa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	945	99.0	200	2	US-09-895-834-5	Sequence 5, Appli
2	945	99.0	200	2	US-09-895-834-7	Sequence 7, Appli
3	940	98.4	200	2	US-09-893-737-268	Sequence 268, Appli
4	940	98.4	203	2	US-09-895-834-2	Sequence 2, Appli
5	940	98.4	203	2	US-09-895-834-12	Sequence 12, Appli
6	940	98.4	219	2	US-09-895-834-9	Sequence 9, Appli
7	83	8.7	567	2	US-09-538-092-1365	Sequence 1365, Appli
8	82	8.6	315	2	US-09-370-398-6	Sequence 6, Appli
9	92	8.6	315	2	US-10-370-190-6	Sequence 6, Appli
10	82	8.6	315	2	US-10-032-902-6	Sequence 6, Appli
11	82	8.6	899	2	US-09-038-092-27	Sequence 27, Appli
12	81.5	8.5	1228	2	US-09-252-991A-17764	Sequence 17764, Appli
13	81	8.5	164	2	US-10-047-047-3099	Sequence 3099, Appli
14	80	8.4	563	1	US-08-051-636-2	Sequence 2, Appli
15	80	8.4	563	4	PCT-US94-05268-2	Sequence 2, Appli
16	79	8.3	315	2	US-08-965-903B-8	Sequence 8, Appli
17	79.5	8.3	315	2	US-09-370-398-3	Sequence 3, Appli
18	79.5	8.3	315	2	US-10-080-190-3	Sequence 3, Appli
19	79.5	8.3	315	2	US-10-082-902-3	Sequence 3, Appli
20	79	8.3	495	2	US-09-712-363-181	Sequence 181, Appli
21	79	8.3	903	2	US-09-758-007-1	Sequence 1, Appli
22	79	8.3	1114	2	US-09-637-145-4	Sequence 4, Appli
23	78.5	8.2	378	2	US-09-724-797-40	Sequence 40, Appli
24	78.5	8.2	780	2	US-09-771-161A-144	Sequence 144, Appli
25	78.5	8.2	942	2	US-08-852-3	Sequence 3, Appli
26	78.5	8.2	942	2	US-09-771-161A-235	Sequence 235, Appli
27	78.5	8.2	942	2	US-09-771-161A-236	Sequence 236, Appli

ALIGNMENTS

RESULT 1
US-09-895-834-5
; Sequence 5, Application US/09895834
; Parent No. 627040
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Fox, Brian A.
; APPLICANT: Gilbert, Teresa
; APPLICANT: Halderman, Betty A.
; APPLICANT: Grant, Francis J.
; FILE REFERENCE: 01-18
; CURRENT APPLICATION NUMBER: US/09-949-016-8542
; PRIORITY APPLICATION NUMBER: 2001-06-29
; PRIORITY FILING DATE: 2001-04-20
; PRIORITY NUMBER: 60/215,446
; PRIORITY FILING DATE: 2000-06-30
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 200
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-895-834-5

Query Match 99.0% ; Score 945; Pred. No. 5 3e-99;
Best Local Similarity 99.4%; Pred. No. 5 3e-99;
Matches 180 ; Mismatches 0 ; Indels 0 ; Gaps 0;

Qy 2 GPVPTSKPTTGGCHIGRKSLSSPQLASKKARDALESILKLNWCSSPVPGNWDL 61
Db 20 GPVPTSKPTTGGCHIGRKSLSSPQLASKKARDALESILKLNWCSSPVPGNWDL 79

Query Match 99.0% ; Score 945; DB 2; Length 200;
Best Local Similarity 99.4%; Pred. No. 5 3e-99;
Matches 180 ; Conserv 0 ; Mismatches 0 ; Indels 0 ; Gaps 0;

Qy 62 RLLQERPVALEAELALTIVKLEAAAGPALEDVQPLTLHHLISOLQRCIOPOPTAG 121
Db 80 RLLQERPVALEAELALTIVKLEAAAGPALEDVQPLTLHHLISOLQRCIOPOPTAG 139

Qy 122 PRPRGLRHWLQLQKPKESAGCLEASYTFNLFRLLTRDLYVADGNLSLRSTHPE 181
Db 140 PRPRGLRHWLQLQKPKESAGCLEASYTFNLFRLLTRDLYVADGNLCLRTSTHPE 199

RESULT 2
US-09-895-834-7

Sequence 7, Application US/09895834
 Parent No. 6927040
 GENERAL INFORMATION:
 APPLICANT: Sheppard, Paul O.
 APPLICANT: Presnell, Scott R.
 APPLICANT: Fox, Brian A.
 APPLICANT: Gilbert, Teresa A.
 APPLICANT: Haldeman, Betty A.
 APPLICANT: Grant, Francis J.
 TITLE OF INVENTION: INTERFERON-LIKE PROTEIN ZCYTO21
 FILE REFERENCE: 01-18
 CURRENT APPLICATION NUMBER: US/09/895,834
 CURRENT FILING DATE: 2001-06-29
 PRIOR APPLICATION NUMBER: 60/285,424
 PRIOR FILING DATE: 2001-04-20
 PRIOR APPLICATION NUMBER: 60/215,446
 PRIOR FILING DATE: 2000-06-30
 NUMBER OF SEQ ID NOS: 16
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO 7
 LENGTH: 200
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-895-834-7

Query Match 99.0%; Score 945; DB 2; Length 200;
 Best Local Similarity 99.4%; Pred. No. 5.3e-99;
 Matches 180; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GPVPTSKPTTGGCHIGRFXKSLSPQELASPKARDALEESLKLKNWSCSSPFPGNWDL 61
 Db 20 GPVPTSKPTTGGCHIGRFXKSLSPQELASPKARDALEESLKLKNWSCSSPFPGNWDL 79

Qy 62 RLLQVERPVALEALALTKVLEAAGPALEVDQPLTLHILSQLQCIQOPTAG 121
 Db 80 RLLQVERPVALEALALTKVLEAAGPALEVDQPLTLHILSQLQCIQOPTAG 139

Qy 122 PRPRGRLHHLRHLQAPKESAGGLEASVTFNLFRLLTRDLYVADGNLSLRTSTHPS 181
 Db 140 PRPRGRLHHLRHLQAPKESAGGLEASVTFNLFRLLTRDLYVADGNLSLRTSTHPS 199

Qy 182 T 182
 Db 200 T 200

RESULT 3
 US-09-893-737-268
 Sequence 268, Application US/09893737
 Patent No. 6922082
 GENERAL INFORMATION:
 APPLICANT: Sheppard, Paul O.
 APPLICANT: Presnell, Scott R.
 TITLE OF INVENTION: MAMMALIAN SECRETED PROTEINS
 FILE REFERENCE: 00-41
 CURRENT APPLICATION NUMBER: US/09/893,737
 CURRENT FILING DATE: 2001-06-28
 PRIOR APPLICATION NUMBER: US 60/215,446
 PRIOR FILING DATE: 2000-06-30
 NUMBER OF SEQ ID NOS: 329
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO 268
 LENGTH: 200
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-03-893-737-268

Query Match 98.4%; Score 940; DB 2; Length 200;
 Best Local Similarity 98.9%; Pred. No. 1.9e-98;
 Matches 179; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GPVPTSKPTTGGCHIGRFXKSLSPQELASPKARDALEESLKLKNWSCSSPFPGNWDL 61
 Db 20 GPVPTSKPTTGGCHIGRFXKSLSPQELASPKARDALEESLKLKNWSCSSPFPGNWDL 79

Qy 62 RLLQVERPVALEALALTKVLEAAGPALEVDQPLTLHILSQLQCIQOPTAG 121
 Db 80 RLLQVERPVALEALALTKVLEAAGPALEVDQPLTLHILSQLQCIQOPTAG 139

Qy 122 PRPRGRLHHLRHLQAPKESAGGLEASVTFNLFRLLTRDLYVADGNLSLRTSTHPS 181
 Db 140 PRPRGRLHHLRHLQAPKESAGGLEASVTFNLFRLLTRDLYVADGNLSLRTSTHPS 199

Qy 182 T 182
 Db 200 T 200

RESULT 4
 US-09-895-834-2
 Sequence 2, Application US/09895834
 Patent No. 6927040
 GENERAL INFORMATION:
 APPLICANT: Sheppard, Paul O.
 APPLICANT: Presnell, Scott R.
 APPLICANT: Fox, Brian A.
 APPLICANT: Gilbert, Teresa A.
 APPLICANT: Haldeman, Betty A.
 APPLICANT: Grant, Francis J.
 TITLE OF INVENTION: INTERFERON-LIKE PROTEIN ZCYTO21
 FILE REFERENCE: 01-18
 CURRENT APPLICATION NUMBER: US/09/895,834
 CURRENT FILING DATE: 2001-06-29
 PRIOR APPLICATION NUMBER: 60/285,424
 PRIOR FILING DATE: 2001-04-20
 PRIOR APPLICATION NUMBER: 60/215,446
 PRIOR FILING DATE: 2000-06-30
 NUMBER OF SEQ ID NOS: 16
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO 2
 LENGTH: 200
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-895-834-2

Query Match 98.4%; Score 940; DB 2; Length 200;
 Best Local Similarity 98.9%; Pred. No. 1.9e-98;
 Matches 179; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GPVPTSKPTTGGCHIGRFXKSLSPQELASPKARDALEESLKLKNWSCSSPFPGNWDL 61
 Db 20 GPVPTSKPTTGGCHIGRFXKSLSPQELASPKARDALEESLKLKNWSCSSPFPGNWDL 79

Qy 62 RLLQVERPVALEALALTKVLEAAGPALEVDQPLTLHILSQLQCIQOPTAG 121
 Db 80 RLLQVERPVALEALALTKVLEAAGPALEVDQPLTLHILSQLQCIQOPTAG 139

Qy 122 PRPRGRLHHLRHLQAPKESAGGLEASVTFNLFRLLTRDLYVADGNLSLRTSTHPS 181
 Db 140 PRPRGRLHHLRHLQAPKESAGGLEASVTFNLFRLLTRDLYVADGNLSLRTSTHPS 199

Qy 182 T 182
 Db 200 T 200

RESULT 5
 US-09-895-834-12
 Sequence 12, Application US/09895834
 Patent No. 6927040
 GENERAL INFORMATION:
 APPLICANT: Sheppard, Paul O.
 APPLICANT: Presnell, Scott R.
 APPLICANT: Fox, Brian A.
 APPLICANT: Gilbert, Teresa A.
 APPLICANT: Haldeman, Betty A.
 APPLICANT: Grant, Francis J.

1 APPLICANT: Grant, Francis J.
 1 TITLE OF INVENTION: INTERFERON-LIKE PROTEIN 2CYT021
 1 FILE REFERENCE: 01-18
 1 CURRENT APPLICATION NUMBER: US/09/895, 834
 1 CURRENT FILING DATE: 2001-06-29
 1 PRIORITY APPLICATION NUMBER: 60/285, 424
 1 PRIORITY FILING DATE: 2001-04-20
 1 PRIORITY APPLICATION NUMBER: 60/215, 446
 1 PRIORITY FILING DATE: 2000-06-30
 1 NUMBER OF SEQ ID NOS: 16
 1 SOFTWARE: FastSEQ for Windows Version 3.0
 1 SEQ ID NO: 12
 1 LENGTH: 203
 1 TYPE: PRT
 1 ORGANISM: Homo sapiens
 1 US-09-895-834-12

Query Match 98.4%; Score 940; DB 2; Length 203;
 Best Local Similarity 98.9%; Pred. No. 2e-98; 1; Indels 0; Gaps 0;
 Matches 179; Conservative

Qy 2 GPVPTSKPTTGGCHICRFKSLSPQEASFKCARDALFESLKLKNWCSSSPVPGNWL 61
 Db 23 GPVPTSKPTTGGCHICRFKSLSPQEASFKCARDALFESLKLKNWCSSSPVPGNWL 82

Qy 62 RLQVREPPVAELAATLKVLEAAAGPALEVDLQPLTHHILSLOQACIOPPTAG 1.21
 Db 83 RLQVREPPVAELAATLKVLEAAAGPALEVDLQPLTHHILSLOQACIOPPTAG 142

Qy 122 PRGRGLHHWLRQEAQPKESAGCLEAVTFNLFRLLTRDLYVADGNLSLRTSTHPS 181
 Db 143 PRGRGLHHWLRQEAQPKESAGCLEAVTFNLFRLLTRDLYVADGNLSLRTSTHPS 202

Qy 182 T 182
 Db 203 T 203

RESULT 6
 US-09-895-834-9
 Sequence 9, Application US/0995834
 Patent No. 692040
 GENERAL INFORMATION
 APPLICANT: Sheppard, Paul O.
 APPLICANT: Presneil, Scott R.
 APPLICANT: Fox, Brian A.
 APPLICANT: Gilber, Teresa
 APPLICANT: Haldeman, Betty A.
 APPLICANT: Grant, Francis J.
 TITLE OF INVENTION: INTERFERON-LIKE PROTEIN 2CYT021
 FILE REFERENCE: 01-18
 CURRENT APPLICATION NUMBER: US/09/895, 834
 CURRENT FILING DATE: 2001-06-29
 PRIORITY APPLICATION NUMBER: 60/285, 424
 PRIORITY FILING DATE: 2001-04-20
 PRIORITY APPLICATION NUMBER: 60/215, 446
 PRIORITY FILING DATE: 2000-06-30
 NUMBER OF SEQ ID NOS: 16
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO: 9
 LENGTH: 219
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-895-834-9

Query Match 98.4%; Score 940; DB 2; Length 219;
 Best Local Similarity 98.9%; Pred. No. 2e-98; 1; Indels 0; Gaps 0;
 Matches 179; Conservative

Qy 2 GPVPTSKPTTGGCHICRFKSLSPQEASFKCARDALFESLKLKNWCSSSPVPGNWL 61
 Db 39 GPVPTSKPTTGGCHICRFKSLSPQEASFKCARDALFESLKLKNWCSSSPVPGNWL 98

Qy 62 RLQVREPPVAELAATLKVLEAAAGPALEVDLQPLTHHILSLOQACIOPPTAG 1.21
 Db 99 RLQVREPPVAELAATLKVLEAAAGPALEVDLQPLTHHILSLOQACIOPPTAG 158

Qy 122 PRGRGLHHWLRQEAQPKESAGCLEAVTFNLFRLLTRDLYVADGNLSLRTSTHPS 181
 Db 159 PRGRGLHHWLRQEAQPKESAGCLEAVTFNLFRLLTRDLYVADGNLSLRTSTHPS 218

Qy 182 T 182
 Db 219 T 219

RESULT 7
 US-09-338-092-1365
 Sequence 1365, Application US/09538092
 Patent No. 6753314
 GENERAL INFORMATION:
 APPLICANT: Giot, Loic
 APPLICANT: Mansfield, Traci A.
 TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
 FILE REFERENCE: 15966-542
 CURRENT FILING DATE: 2000-03-29
 PRIORITY APPLICATION NUMBER: 60/127, 352
 PRIORITY FILING DATE: 1999-04-01
 PRIORITY APPLICATION NUMBER: 60/178, 965
 PRIORITY FILING DATE: 2000-02-01
 NUMBER OF SEQ ID NOS: 1387
 SOFTWARE: CurapateSeqFormatter Version 0.9
 SEQ ID NO: 1365
 LENGTH: 567
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (0)-(10)
 OTHER INFORMATION: Polypeptide Accession Number Q92696
 US-09-338-092-1365

Query Match 98.7%; Score 83; DB 2; Length 567;
 Best Local Similarity 25.6%; Pred. No. 1.4%;
 Matches 50; Conservative 16; Mismatches 59; Indels 70; Gaps 9;

Qy 25 SPOELASFKKAR-DALEESLKLKNWCSSSPVPGNWLQYERPVVA-LRAELAATLKK 82
 Db 81 SPEELALVKAELGFLESCLRV----NPKSYGTTWHRCLWLGRLEPNWTRELCAR 134

Qy 83 VLE------AAGPALEVDLQPLTHL-----HILSLOQACIOPQ 117
 Db 135 FLEVDERNFHCMDDYRREPTAQAVPPABEALFTDSLTRNFNYSWHYRSCLPQLPQ 194

Qy 118 PTAGPRGRGL-----HMLHRLQEPKKESSAGCL-- 147
 Db 195 PDSG----PGRLPEDVLLKELELVQNAFFPDNQDSAWFYHRL--LGRADPDALRCLHV 250

Qy 148 ---EASYTFNLFRLL 159
 Db 251 SRDEAATVFSRPL 265

RESULT 8
 US-09-370-398-6
 Sequence 6, Application US/09370398
 Patent No. 6423682
 GENERAL INFORMATION:
 APPLICANT: Ballinger, Dennis G.
 APPLICANT: Montgomery, Julie R.
 TITLE OF INVENTION: Growth Factor Antagonist Materials and Methods
 FILE REFERENCE: 28110/35878
 CURRENT APPLICATION NUMBER: US/09/370, 398
 CURRENT FILING DATE: 1998-08-06
 NUMBER OF SEQ ID NOS: 13

US-10-082-902-6

SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 6
LENGTH: 315
TYPE: PRT
ORGANISM: *Mus musculus*
US-10-09-370-398-6

Query Match 8.6%; Score 82; DB 2; Length 315;
Best Local Similarity 28.6%; Pred. No. 0.79; Gaps 3;
Matches 30; Conservative 13; Mismatches 48; Indels 14; Gaps 3;

Qy 90 PALEVDLQPLHTLHILSQLQA-----CIOQOPTAGPRGRGLHHLHILSQLQA 138
Db 28 PDPDRDLTQQHVLS-LDQPAIRNTNEYTEGPTVPRGKPKAPRSTQHKHLHGL 85

Qy 139 PKEESAGCLEASVTNFLFRLLTDLKLYADGN-LSLRSTSTHPEST 182
Db 86 PEHRQPRLQPSQVHSSRAPLSRSISTVSSGSRSSRTSSSS 130

RESULT 11
US-09-538-092-27
Sequence 27 Application US/09538092
Patent No. 675314
GENERAL INFORMATION:
APPLICANT: Giot, Loic
APPLICANT: Mansfield, Traci A.
FILE REFERENCE: 15966-542
CURRENT APPLICATION NUMBER: US/09/538.092
CURRENT FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: 60/127,352
PRIOR FILING DATE: 1999-04-01
PRIOR APPLICATION NUMBER: 60/178,965
PRIOR FILING DATE: 2000-02-01
NUMBER OF SEQ ID NOS: 1387
SOFTWARE: CuraPatSeqFormatter Version 0.9
SEQ ID NO: 27
LENGTH: 899
TYPE: PRT
ORGANISM: *Saccharomyces cerevisiae*
FEATURE:
NAME/KEY: misc_feature
LOCATION: (01.00)
OTHER INFORMATION: Polypeptide Accession Number YBR055C
US-09-538-092-27

Query Match 8.6%; Score 82; DB 2; Length 899;
Best Local Similarity 22.6%; Pred. No. 3.4;
Matches 38; Conservative 27; Mismatches 61; Indels 42; Gaps 8;

Qy 33 KCARDALEESLKLKNWCSSPVPGNDL-RLQVRL-----PVA 72
Db 131 RNKRNRLQEQLNRKTYAAPSLSLPGNDLNLKLTBERKLQLQSNIDENLQLQNSNPIQ 190

Qy 73 LEABLAAT-LKVEAAGAAGPALEDVLDQPLHILHILSQLQACIOPQPTAGPRGRGLH 130
Db 191 VNKPNAAATDALSYKLDLENDRYNSLSATLDEQKMTILSKYRKAQPT-----NFGQ 243

Qy 131 WL-HRQDAPKKESA-----GCL-----ASVTFFNLFRLLTDLKLY 165
Db 244 WIASARLLEEAKPKSVAKKIIENGQBCPRSSDIWLNLIRLHESDVHY 291

RESULT 12
US-09-52-991A-17764
Sequence 17764, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfeld et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOURIDYLIC ACID ET AL.
FILE REFERENCE: 107196-136
CURRENT APPLICATION NUMBER: US/09/252.991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190

SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 6
LENGTH: 315
TYPE: PRT
ORGANISM: *Mus musculus*
US-10-082-902-6

Query Match 8.6%; Score 82; DB 2; Length 315;
Best Local Similarity 28.6%; Pred. No. 0.79; Gaps 3;
Matches 30; Conservative 13; Mismatches 48; Indels 14; Gaps 3;

Qy 90 PALEVDLQPLHTLHILSQLQA-----CIOQOPTAGPRGRGLHHLHILSQLQA 138
Db 28 PDPDRDLTQQHVLS-LDQPAIRNTNEYTEGPTVPRGKPKAPRSTQHKHLHGL 85

Qy 139 PKEESAGCLEASVTNFLFRLLTDLKLYADGN-LSLRSTSTHPEST 182
Db 86 PEHRQPRLQPSQVHSSRAPLSRSISTVSSGSRSSRTSSSS 130

RESULT 13
US-10-082-902-6
Sequence 6, Application US/10082902
Patent No. 6706871
GENERAL INFORMATION:
APPLICANT: Ballinger, Dennis G.
APPLICANT: Montgomery, Julie R.
TITLE OF INVENTION: Growth Factor Antagonist Materials and Methods
FILE REFERENCE: 28110/35878
CURRENT APPLICATION NUMBER: US/10/082,902
CURRENT FILING DATE: 2002-02-26
PRIOR APPLICATION NUMBER: US/09/370,398
PRIOR FILING DATE: 1998-08-06
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 6
LENGTH: 315
TYPE: PRT
ORGANISM: *Mus musculus*
US-10-09-090-190-6

Query Match 8.6%; Score 82; DB 2; Length 315;
Best Local Similarity 28.6%; Pred. No. 0.79; Gaps 3;
Matches 30; Conservative 13; Mismatches 48; Indels 14; Gaps 3;

Qy 90 PALEVDLQPLHTLHILSQLQA-----CIOQOPTAGPRGRGLHHLHILSQLQA 138
Db 28 PDPDRDLTQQHVLS-LDQPAIRNTNEYTEGPTVPRGKPKAPRSTQHKHLHGL 85

Qy 139 PKEESAGCLEASVTNFLFRLLTDLKLYADGN-LSLRSTSTHPEST 182
Db 86 PEHRQPRLQPSQVHSSRAPLSRSISTVSSGSRSSRTSSSS 130

RESULT 14
US-09-52-991A-17764
Sequence 17764, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfeld et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOURIDYLIC ACID ET AL.
FILE REFERENCE: 107196-136
CURRENT APPLICATION NUMBER: US/09/252.991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27
 NUMBER OF SEQ ID NOS: 33142
 SEQ ID NO: 17764
 LENGTH: 1228
 TYPE: PRT
 ORGANISM: *Pseudomonas aeruginosa*
 FEATURE:
 NAME/KEY: UNSURE
 LOCATION: (17)
 OTHER INFORMATION: Identity of amino acid at the above locations are unknown.
 US-09-252-91A-17764

Query Match 8.5%; Score 81.5; DB 2; Length 1228;
 Best Local Similarity 33.0%; Pred. No. 5.9;
 Matches 32; Conservative 5; Mismatches 33; Indels 27; Gaps 5;
 Qy 56 PGNWDLR-----LQYRERPVAALEALTLKVLEAAAGPALEVDLQPLTLHHL 107
 Db 738 PGRADLRRPADRRHHLPLRRRSRVRARRS-----GHARGQA - PVLDAFGHSAH--- 784
 Qy 1068 SOLQACIQQP---TAGPRPRGLRHLWHLRLOEAKP 140
 Db 785 -LRAAVPQRGPGRADRRRLRHLRYHLRHLPR 819

RESULT 13
 US-10-104-047-3099

Sequence 3099, Application US/10104047

Patent No. 6913241

GENERAL INFORMATION

APPLICANT: HELIX RESEARCH INSTITUTE

FILE REFERENCE: HI-A0105

CURRENT APPLICATION NUMBER: US/10/104,047

PRIOR APPLICATION NUMBER:

PRIOR FILING DATE:

NUMBER OF SEQ ID NOS: 4096

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO: 3099

LENGTH: 164

TYPE: PRT

ORGANISM: *Homo sapiens*

US-10-104-047-3099

Query Match 8.5%; Score 81; DB 2; Length 164;

Best Local Similarity 24.3%; Pred. No. 0.41; Mismatches 59; Indels 48; Gaps 9;

Matches 41; Conservative 21; Mismatches 59;

Qy 1 MGPVPTSKPTTGGKCHGRFKSLSPQLASFKK---ARDALESLKLKWNCSSPVFP 55

Db 6 LSPGPVSRVLAAPSCPFG---LLEEECHTLEREIILQRCLEEEYLR-----PCH 53

Qy 56 PGNWDLR---LQYRERPVAALEALTLKVLEAAAGPALEVDLQPLTLHHL 112

Db 54 PSEAALEPTLAELKEQQAMEQE-----LQASVGPSCV---SPNTRQRPLGSSTQGL 102

Qy 113 -----CIOPTPTAGP---RPGGR---LHHWHLRQLQEAQKCESA 144

Db 103 RPPPLPLCCGVAPLQOCLPAPPLEPYLRRPGQSATHRGQCSRQCSPREGAA 151

RESULT 14
 US-08-061-636-2

Sequence 2, Application US/08061636

Patent No. 5858765

GENERAL INFORMATION

APPLICANT: Myers, Alan M.

APPLICANT: Madoule, Pascal

TITLE OF INVENTION: Constitutive Pseudohyphal Growth Yeast

TITLE OF INVENTION: Mutants

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: Schwegman, Lundberg & Woessner
 STREET: 3500 IDS Center, 80 South Eighth Street
 CITY: Minneapolis
 STATE: MN USA

ZIP: 55402

GENERAL INFORMATION

APPLICANT: Myers, Alan M.

APPLICANT: Madoule, Pascal

TITLE OF INVENTION: Constitutive Pseudohyphal Growth Yeast

TITLE OF INVENTION: Mutants

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lundberg, Lundberg & Woessner
 STREET: 3500 IDS Center, 80 South Eighth Street
 CITY: Minneapolis
 STATE: MN USA

ZIP: 55402

GENERAL INFORMATION

APPLICANT: Myers, Alan M.

APPLICANT: Madoule, Pascal

TITLE OF INVENTION: Constitutive Pseudohyphal Growth Yeast

TITLE OF INVENTION: Mutants

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: Merchant & Gould
 STREET: 3100 No. 585765west Center
 CITY: Minneapolis
 STATE: MN USA

COUNTRY: USA

ZIP: 55402-4131

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

APPLICATION NUMBER: US/08/061,636

CLASSIFICATION: 12-RAY-1993

ATTORNEY/AGENT INFORMATION:

NAME: Muetting, Ann M.

REGISTRATION NUMBER: 33,977

REFERENCE/DOCKET NUMBER: 9399.38-US01

TELECOMMUNICATION INFORMATION:

TELEPHONE: 612-332-5300

TELEFAX: 612-332-9081

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 563 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-061-636-2

Query Match 8.4%; Score 80; DB 1; Length 563;
 Best Local Similarity 23.5%; Pred. No. 3;
 Matches 38; Conservative 20; Mismatches 44; Indels 60; Gaps 8;

Query Match 8.4%; Score 80; DB 1; Length 563;
 Best Local Similarity 23.5%; Pred. No. 3;
 Matches 38; Conservative 20; Mismatches 44; Indels 60; Gaps 8;
 Qy 16 CHIGRFKSLSPQELASFKKARDALLESLKLKWNCSSSPVPFGNMDLRLQYRERYALEA 75
 Db 319 CHLGNSK-----RDFVTFGEKLDIWSLGVLY-----CLLYNELPFFGEN 358
 Qy 76 EIALTUKVLEAA---GAPEADVL-----DOPLHTLHHI 106
 Db 359 EFETYKIIIEVLSLSKINGTLVYKRLLEKDVTLRISIOLVYKLSRDQPIDSRNH- 417
 Qy 107 LSQL-QRCIOPPTAGPFRPRR-GRAFHWHRLQEAQKCESAG 145
 Db 418 -SQISSLSSVNPVTRTEGVRRFFGRL-----LTKGKXKKTSG 452

RESULT 15
 PCT-US94-052268-2

SEQUENCE 2, APPLICATION PC/US94052268

GENERAL INFORMATION:

APPLICANT: Iowa State University Research Foundation, Inc.

APPLICANT: Institut Pasteur

APPLICANT: Institut National de la Sant et de la Recherche M dicale

APPLICANT: Recherche M dicale

APPLICANT: Myers, Alan M.

APPLICANT: Madoule, Pascal

TITLE OF INVENTION: Constitutive Pseudohyphal Growth Yeast

TITLE OF INVENTION: Mutants

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lundberg, Lundberg & Woessner
 STREET: 3500 IDS Center, 80 South Eighth Street
 CITY: Minneapolis
 STATE: MN USA

ZIP: 55402

GENERAL INFORMATION

APPLICANT: Myers, Alan M.

APPLICANT: Madoule, Pascal

TITLE OF INVENTION: Constitutive Pseudohyphal Growth Yeast

TITLE OF INVENTION: Mutants

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: Schwegman, Lundberg & Woessner
 STREET: 3500 IDS Center, 80 South Eighth Street
 CITY: Minneapolis
 STATE: MN USA

ZIP: 55402

GENERAL INFORMATION

APPLICANT: Myers, Alan M.

APPLICANT: Madoule, Pascal

TITLE OF INVENTION: Constitutive Pseudohyphal Growth Yeast

TITLE OF INVENTION: Mutants

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/05268
FILING DATE: 12 MAY 1993
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08 /061, 636
FILING DATE: 12 MAY 1993
ATTORNEY/AGENT INFORMATION:
NAME: Muetting, Ann M. and Raasch, K.
REGISTRATION NUMBER: 33,977 and 35,
REFERENCE/DOCKET NUMBER: 900-38W0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-319-0331
TELEFAX: 612-339-3061
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 563 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ID: US4-05268-2

Search completed: December 29, 2005, 14:00:44
Total time: 15:20:00

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OM protein - protein search, using sw model

Run on: December 29, 2005, 13:59:18 ; Search time 164 Seconds
(without alignments)

463.689 Million cell updates/sec

Title: US-10-691-923-34

Perfect score: 955

Sequence: 1 MGPVPTSKPTTIGKGCHIGR.....LKVADGNLSLRTSTHPEST 182

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0*

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:
1: /cnr2_6/ptodata/1/pubpaas/us07_PUBCOMB_pep:
2: /cnr2_6/ptodata/1/pubpaas/us08_PUBCOMB_pep:
3: /cnr2_6/ptodata/1/pubpaas/us09_PUBCOMB_pep:
4: /cnr2_6/ptodata/1/pubpaas/us10A_PUBCOMB_pep:
5: /cnr2_6/ptodata/1/pubpaas/us10B_PUBCOMB_pep:
6: /cnr2_6/ptodata/1/pubpaas/us11_PUBCOMB_pep:
*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	955	100.0	182	4	US-10-691-923-34	Sequence 34, Appl
2	955	100.0	182	5	US-10-914-772-29	Sequence 29, Appl
3	951	99.6	182	5	US-10-914-772-41	Sequence 41, Appl
4	950	99.5	181	4	US-10-691-923-32	Sequence 32, Appl
5	950	99.5	181	5	US-10-914-772-27	Sequence 27, Appl
6	950	99.5	182	4	US-10-691-923-38	Sequence 38, Appl
7	950	99.3	182	5	US-10-914-772-15	Sequence 15, Appl
8	948	99.3	183	5	US-10-914-772-15	Sequence 155, Appl
9	947	99.2	183	5	US-10-914-772-155	Sequence 40, Appl
10	946	99.1	181	5	US-10-914-772-40	Sequence 85, Appl
11	946	99.1	182	5	US-10-914-772-85	Sequence 161, Appl
12	946	99.1	185	5	US-10-914-772-161	Sequence 89, Appl
13	945	99.0	182	5	US-10-914-772-89	Sequence 5, Appl
14	945	99.0	200	3	US-09-895-834-5	Sequence 7, Appl
15	945	99.0	200	3	US-09-895-834-7	Sequence 4, Appl
16	945	99.0	200	4	US-10-691-923-20	Sequence 20, Appl
17	945	99.0	200	4	US-10-790-996-5	Sequence 5, Appl
18	945	99.0	200	4	US-10-790-996-7	Sequence 7, Appl
19	945	99.0	200	5	US-10-928-539-5	Sequence 5, Appl
20	945	99.0	200	5	US-10-928-539-7	Sequence 7, Appl
21	945	99.0	200	5	US-10-914-772-4	Sequence 4, Appl
22	945	99.0	200	5	US-10-927-891-5	Sequence 5, Appl
23	945	99.0	200	5	US-10-927-891-7	Sequence 7, Appl
24	945	99.0	200	5	US-10-927-815-5	Sequence 5, Appl
25	945	99.0	200	5	US-10-927-815-7	Sequence 7, Appl
26	944	98.8	182	5	US-10-914-772-05	Sequence 105, Appl
27	941	98.5	181	5	US-10-914-772-83	Sequence 83, Appl

ALIGNMENTS

RESULT 1
US-10-691-923-34
; Sequence 34, Application US-106919231
; Publication No. US20040138122A1
; GENERAL INFORMATION:
; APPLICANT: Klucher, Kevin M.
; APPLICANT: Sivakumar, Pallavur V.
; APPLICANT: Kirdsogel, Wayne R.
; APPLICANT: Henderson, Katherine E.
; TITLE OF INVENTION: METHODS FOR TREATING VIRAL INFECTION
; TITLE OF INVENTION: USING IL-28 AND IL-29
; CURRENT APPLICATION NUMBER: US/10/691,923
; CURRENT FILING DATE: 2003-10-23
; PRIOR APPLICATION NUMBER: US 60/420,714
; PRIOR FILING DATE: 2002-10-23
; PRIOR APPLICATION NUMBER: US 60/463,939
; PRIOR FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: US 60/420,713
; PRIOR FILING DATE: 2002-10-23
; PRIOR APPLICATION NUMBER: US 60/463,982
; PRIOR FILING DATE: 2003-04-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSEQ For Windows Version 4.0
; SEQ ID NO: 34
; LENGTH: 182
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: met IL-29 mutant C1728
; US-10-691-923-34

Query Match 100.0%; Score 955; DB 4; Length 182;
Best Local Similarity 100.0%; Pred. No. 1.4e-86; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGPPVPTSKPTTIGKGCHIGRGRFKSLSPQELASFKKARDALESLKLKWNWSLQLQACTQOPTA 120
Db 1 MGPPVPTSKPTTIGKGCHIGRGRFKSLSPQELASFKKARDALESLKLKWNWSLQLQACTQOPTA 120
Qy 1 LRLQVRERPVAAELALITLKVLEAAGPALEVDLQDPLTHLHILSQLQACTQOPTA 120
Db 1 LRLQVRERPVAAELALITLKVLEAAGPALEVDLQDPLTHLHILSQLQACTQOPTA 120
Qy 1 GPRGRGLHHWHLHRLQERPKKESAGCLESATVNFLFRDLYKVAQDNLSLRTSTHPE 180
Db 1 GPRGRGLHHWHLHRLQERPKKESAGCLESATVNFLFRDLYKVAQDNLSLRTSTHPE 180
Qy 181 ST 182

Query Match 99.5%; Score 950; DB 4; Length 181;
 Best Local Similarity 100.0%; Prd. No. 4.3e-06;
 Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 SEQ ID NO: 121 PRPGRLLHHLRQEAQPKESAGCLEASVTENLFRLLTRDKYVADGNLSLRSTTHES 180

Db 181 ST 181

RESULT 6
 Sequence 38, Application US/10691923
 Publication No. US20040138122A1
 GENERAL INFORMATION:
 APPLICANT: Klucher, Kevin M.
 APPLICANT: Sivakumar, Pallavur V.
 APPLICANT: Kindvoge, Wayne R.
 APPLICANT: Henderson, Katherine E.
 TITLE OF INVENTION: METHODS FOR TREATING VIRAL INFECTION
 TITLE OF INVENTION: USING IL-28 AND IL-29
 FILE REFERENCE: 02-24
 CURRENT APPLICATION NUMBER: US/10/691,923
 CURRENT FILING DATE: 2003-10-23
 PRIOR APPLICATION NUMBER: US 60/420,714
 PRIOR FILING DATE: 2002-10-23
 PRIOR APPLICATION NUMBER: US 60/463,939
 PRIOR FILING DATE: 2003-04-18
 PRIOR APPLICATION NUMBER: US 60/420,713
 PRIOR FILING DATE: 2002-10-23
 PRIOR APPLICATION NUMBER: US 60/463,982
 NUMBER OF SEQ ID NOS: 40
 SEQ ID NO: 38
 LENGTH: 182
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: FastSEQ for Windows Version 4.0
 US-10-691-923-38

Query Match 99.5%; Score 950; DB 4; Length 182;
 Best Local Similarity 99.5%; Prd. No. 4.3e-06;
 Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 SEQ ID NO: 122 PRPGRLLHHLRQEAQPKESAGCLEASVTENLFRLLTRDKYVADGNLSLRSTTHES 181

Db 181 ST 182

RESULT 5
 Sequence 27, Application US/10914772
 Publication No. US20050037012A1
 GENERAL INFORMATION:
 APPLICANT: Brady, Lowell J.
 APPLICANT: Klucher, Kevin M.
 APPLICANT: Chan, Chung
 APPLICANT: Dong, Dennis L.
 APPLICANT: Liu, Hong Y.
 APPLICANT: Sheppard, Paul O.
 APPLICANT: Bokowski, Thomas R.
 TITLE OF INVENTION: HOMOGENEOUS PREPARATIONS OF IL-28 AND
 TITLE OF INVENTION: IL-29
 FILE REFERENCE: 03-10
 CURRENT APPLICATION NUMBER: US/10/914,772
 CURRENT FILING DATE: 2004-01-09
 PRIOR APPLICATION NUMBER: US 60/433,194
 PRIOR FILING DATE: 2003-08-07
 PRIOR APPLICATION NUMBER: US 60/551,841
 PRIOR FILING DATE: 2004-03-10
 PRIOR APPLICATION NUMBER: US 60/559,142
 PRIOR FILING DATE: 2004-04-02
 NUMBER OF SEQ ID NOS: 161
 SEQ ID NO: 27
 LENGTH: 181
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: IL-29 mutant C171S
 US-10-914-772-27

Query Match 99.5%; Score 950; DB 5; Length 181;
 Best Local Similarity 100.0%; Prd. No. 4.3e-06;
 Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 SEQ ID NO: 123 PRPGRLLHHLRQEAQPKESAGCLEASVTENLFRLLTRDKYVADGNLSLRSTTHES 180

Db 181 ST 182

RESULT 7
 Sequence 15, Application US/10914772
 Publication No. US20050037012A1
 GENERAL INFORMATION:
 APPLICANT: Brady, Lowell J.
 APPLICANT: Klucher, Kevin M.
 APPLICANT: Chan, Chung
 APPLICANT: Dong, Dennis L.
 APPLICANT: Liu, Hong Y.
 APPLICANT: Sheppard, Paul O.
 APPLICANT: Bokowski, Thomas R.
 TITLE OF INVENTION: HOMOGENEOUS PREPARATIONS OF IL-28 AND
 TITLE OF INVENTION: IL-29
 FILE REFERENCE: 03-10
 CURRENT APPLICATION NUMBER: US/10/914,772
 CURRENT FILING DATE: 2004-08-09

Db 122 GPRGRGLHHWLRQEAPEKESAGCLEASVTNLFRLTRDKVADGNLXLRSTHPE 181
 Qy 181 ST 182
 Db 182 ST 183

RESULT 10
 US-10-914-772-40
 Sequence 40, Application US/10914772
 Publication No. US20050037012A1
 GENERAL INFORMATION:
 APPLICANT: Brady, Lowell J.
 APPLICANT: Klucher, Kevin M.
 APPLICANT: Dong, Dennis L.
 APPLICANT: Liu, Hong Y.
 APPLICANT: Sheppard, Paul O.
 APPLICANT: Bukiowski, Thomas R.
 TITLE OF INVENTION: HOMOGENEOUS PREPARATIONS OF IL-28 AND
 FILE REFERENCE: 03-10
 CURRENT APPLICATION NUMBER: US/10/914,772
 CURRENT FILING DATE: 2004-08-09
 PRIORITY APPLICATION NUMBER: US 60/493,194
 PRIORITY FILING DATE: 2003-08-07
 PRIORITY APPLICATION NUMBER: US 60/551,841
 PRIORITY FILING DATE: 2004-03-10
 PRIORITY APPLICATION NUMBER: US 60/559,142
 PRIORITY FILING DATE: 2004-04-02
 NUMBER OF SEQ ID NOS: 161
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 85
 LENGTH: 182
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Met IL29 mutant Asp170, C172X
 FEATURE:
 NAME/KEY: VARIANT
 LOCATION: (172) .. (172)
 OTHER INFORMATION: Xaa = Ser, Ala, Thr, Val, or Asn
 US-10-914-772-85

Query Match 99.1%; Score 946; DB 5; Length 182;
 Best Local Similarity 98.9%; Pred. No. 1..1e-85;
 Matches 180; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MGPPTKPTTGGKCHIGRKFLSPQELASFKKARDALEESKLKWNWSSPVPGNWD 60
 Db 1 MGPPTKPTTGGKCHIGRKFLSPQELASFKKARDALEESKLKWNWSSPVPGNWD 60

Qy 61 LRLIQVRRPVVAELALTLKVLEAAGPALEVDLQPLHTLHILSLSQACTQOPQTA 120
 Db 61 LRLIQVRRPVVAELALTLKVLEAAGPALEVDLQPLHTLHILSLSQACTQOPQTA 120

Qy 121 GPRGRGLHHWLRQEAPEKESAGCLEASVTNLFRLTRDKVADGNLSLRSTHPE 180
 Db 121 GPRGRGLHHWLRQEAPEKESAGCLEASVTNLFRLTRDKVADGNLSLRSTHPE 180

RESULT 12
 US-10-914-772-161
 Sequence 161, Application US/10914772
 Publication No. US20050037012A1
 GENERAL INFORMATION:
 APPLICANT: Brady, Lowell J.
 APPLICANT: Klucher, Kevin M.
 APPLICANT: Chan, Chung
 APPLICANT: Dong, Dennis L.
 APPLICANT: Liu, Hong Y.
 APPLICANT: Sheppard, Paul O.
 APPLICANT: Bukiowski, Thomas R.
 TITLE OF INVENTION: HOMOGENEOUS PREPARATIONS OF IL-28 AND
 FILE REFERENCE: 03-10
 CURRENT APPLICATION NUMBER: US/10/914,772
 CURRENT FILING DATE: 2004-08-09
 PRIORITY APPLICATION NUMBER: US 60/493,194
 PRIORITY FILING DATE: 2003-08-07
 PRIORITY APPLICATION NUMBER: US 60/551,841
 PRIORITY FILING DATE: 2004-03-10
 PRIORITY APPLICATION NUMBER: US 60/559,142
 PRIORITY FILING DATE: 2004-04-02

RESULT 11
 US-10-914-772-85
 Sequence 85, Application US/10914772
 Publication No. US20050037012A1
 GENERAL INFORMATION:
 APPLICANT: Brady, Lowell J.
 APPLICANT: Klucher, Kevin M.
 APPLICANT: Chan, Chung

NUMBER OF SEQ ID NOS: 161
 ; SEQ ID NO: 161
 ; LENGTH: 185
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE: OTHER INFORMATION: IL-29 Glu, Ala, and Glu inserted after N-terminal
 ; OTHER INFORMATION: Met, C17X
 ; FEATURE: NAME/KEY: VARIANT
 ; LOCATION: (175) .. (175)
 ; OTHER INFORMATION: Xaa = Ser, Ala, Thr, Val, or Asn
 us-10-914-772-161

Query Match 99.0%; Score 945; DB 5; Length 182;
 Best Local Similarity 98.9%; Pred. No. 1.4e-85;
 Matches 180; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MGPVPTSKPTTGKGCCHIGRFKSLSPQELASFKKARDALEESLKLKWNCSSSPVFPGNWD 60
 Db 1 MGPVPTSKPTTGKGCCHIGRFKSLSPQELASFKKARDALEESLKLKWNCSSSPVFPGNWD 60

Qy 61 RLLOQERPVALEELALTLKVLEAAAGPALEDVLDQPLHTLHILSOLQACIOPPTA 120
 Db 61 RLLOQERPVALEELALTLKVLEAAAGPALEDVLDQPLHTLHILSOLQACIOPPTA 120

Qy 121 GPRGRGLHHWHLRLOEAPKESAGCLEASVTNLFRLLTRDLYVADGNLRLSTHPE 180
 Db 121 GPRGRGLHHWHLRLOEAPKESAGCLEASVTNLFRLLTRDLYVADGNLRLSTHPE 180

Query Match 99.1%; Score 946; DB 5; Length 185;
 Best Local Similarity 99.4%; Pred. No. 1.1e-85;
 Matches 180; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 181 ST 182
 Db 181 ST 182

Qy 2 GPVPTSKPTTGKGCCHIGRFKSLSPQELASFKKARDALEESLKLKWNCSSSPVFPGNWD 61
 Db 5 GPVPTSKPTTGKGCCHIGRFKSLSPQELASFKKARDALEESLKLKWNCSSSPVFPGNWD 64

RESULT 14
 US-09-895-834-5
 ; Sequence 5, Application US/09895834
 ; Publication No. US20020039763A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Sheppard, Paul O.
 ; APPLICANT: Presnell, Scott R.
 ; APPLICANT: Fox, Brian A.
 ; APPLICANT: Gilbert, Terese A.
 ; APPLICANT: Halderman, Betty A.
 ; APPLICANT: Grant, Francis J.
 ; TITLE OF INVENTION: INTERFERON-LIKE PROTEIN CYTO21
 ; FILE REFERENCE: 01-18

CURRENT APPLICATION NUMBER: US/09/895, 834
 CURRENT FILING DATE: 2001-06-29
 PRIOR APPLICATION NUMBER: 60/285, 424
 PRIOR FILING DATE: 2001-04-20
 PRIOR APPLICATION NUMBER: 60/215, 446
 PRIOR FILING DATE: 2000-06-30
 NUMBER OF SEQ ID NOS: 16
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO 5
 LENGTH: 200
 TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-895-834-5

Query Match 99.0%; Score 945; DB 3; Length 200;
 Best Local Similarity 99.4%; Pred. No. 1.5e-85;
 Matches 180; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GPVPTSKPTTGKGCCHIGRFKSLSPQELASFKKARDALEESLKLKWNCSSSPVFPGNWD 61
 Db 20 GPVPTSKPTTGKGCCHIGRFKSLSPQELASFKKARDALEESLKLKWNCSSSPVFPGNWD 79

Qy 62 RLLOQERPVALEELALTLKVLEAAAGPALEDVLDQPLHTLHILSOLQACIOPPTAG 121
 Db 80 RLLOQERPVALEELALTLKVLEAAAGPALEDVLDQPLHTLHILSOLQACIOPPTAG 139

Qy 122 GPRGRGLHHWHLRLOEAPKESAGCLEASVTNLFRLLTRDLYVADGNLRLSTHPE 181
 Db 140 GPRGRGLHHWHLRLOEAPKESAGCLEASVTNLFRLLTRDLYVADGNLRLSTHPE 199

RESULT 15
 US-09-895-834-7
 ; Sequence 7, Application US/09895834
 ; Publication No. US20020039763A1

Qy 182 T 182
 Db 200 T 200

OTHER INFORMATION: Met IL29 mutant Trp, Asn170, C172X
 ; FEATURE: NAME/KEY: VARIANT
 ; LOCATION: (172) .. (172)
 ; OTHER INFORMATION: Xaa = Ser, Ala, Thr, Val, or Asn
 us-10-914-772-89

GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
APPLICANT: Presnell, Scott R.
APPLICANT: Fox, Brian A.
APPLICANT: Gilbert, Teresa
APPLICANT: Haldeman, Betty A.
APPLICANT: Grant, Francis J.
TITLE OF INVENTION: INTERPERSON-LIKE PROTEIN ZCYTO21
FILE REFERENCE: 01-18
CURRENT APPLICATION NUMBER: US/09/995, 834
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: 60/285, 424
PRIOR FILING DATE: 2001-04-20
PRIOR APPLICATION NUMBER: 60/215, 446
PRIOR FILING DATE: 2000-06-30
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO: 7
LENGTH: 200
TYPE: PRT
ORGANISM: Homo sapiens
US-09-895-834-7

	Query Match	Score	DB	Length
Qy	Best Local Similarity	99.0%	3	200;
Qy	Matches 180; Conservative	99.4%	Pred. No. 1.5e-85;	
Qy	0; Mismatches	1;	Indels	0;
Qy	GPIPTSKPTTGGKCHIGRKFKLSPQELASFKKARDALEEESLKLKNWQCSSPVPGNIDL	61		
Db	20 GPyPTSKPTTGGKCHIGRKFKLSPQELASFKKARDALEEESLKLKNWQCSSPVPGNIDL	79		
Qy	62 RLLQYRERPVALEAELAATLKVLEAAAGPALEVDLQDPLHTLHISLQACIQOPPAG	121		
Db	80 RLLQYRERPVALEAELAATLKVLEAAAGPALEVDLQDPLHTLHISLQACIQOPPAG	139		
Qy	122 PRPRGRLLHHLHRLQEAQKKEASAGGLEASYTFLNFRLLTRDLKYVADGNLSRTSTHPS	181		
Db	140 PRPRGRLLHHLHRLQEAQKKEASAGGLEASYTFLNFRLLTRDLKYVADGNLCLRTSTHPS	199		
Qy	182 T 182			
Db	200 T 200			

Search completed: December 29, 2005, 14:13:28
Job time : 165 secs